

SEQUENCE LISTING

<110> Patience, Clive

<120> Gamma Herpes Virus DNA and Methods of Use

<130> 61750-379

<150> US/09/612,204

<151> 2000-07-07

<150> US/60/142,736

<151> 1999-07-08

<150> US/60/168,532

<151> 1999-12-02

<160> 55

<170> PatentIn version 3.0

<210> 1

<211> 585

<212> DNA

<213> artificial

<220>

<223> Fragment from Swine Gamma Herpesvirus DNA coding for glycoprotein B envelope protein

<400> 1

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agcatgatt	acaatagacc	cgtatcagcc	aaaagaatag	gagatgtcat	180
aactgtattt	tggtagacca	aaccagtgtc	tcattacata	aaagtctcag	240
gcatcgatg	aaaagtgcct	ctctagaccc	ccagtgacat	ttaagtttat	300
actatttaca	aaggcaact	aggagtcaat	aatgagattc	tcttaaccac	360
gaaacatgtc	aggaaaacac	tgagtattac	ttcaggcaa	agacagacat	420
aaaaactatg	agcattgaa	gactgtgcct	ttatctcgatc	tcaccacact	480
atagccctta	atttacact	attggagaat	gttgacttta	aagtatttgc	540
agggacgaga	agaggcttag	taatgtctt	gacattgaaa	caatg	585

<210> 2

<211> 195

<212> PRT

<213> artificial

<220>

<223> Deduced amino acid sequence derived from the first open reading frame of the DNA of SEQ ID NO:

<400> 2

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1															15

Trp Cys Arg Glu Gln His Arg Ala Ala Leu Val Trp Asn Glu Leu Ser

14
13
12
11
10
9
8
7
6
5
4
3
2
1

20

25

30

Lys Ile Asn Pro Thr Ser Val Met Ser Met Ile Tyr Asn Arg Pro Val
35 40 45

Ser Ala Lys Arg Ile Gly Asp Val Ile Ser Val Ser Asn Cys Ile Val
50 55 60

Val Asp Gln Thr Ser Val Ser Leu His Lys Ser Leu Arg Leu Leu Ser
65 70 75 80

Ala Ser Asp Glu Lys Cys Phe Ser Arg Pro Pro Val Thr Phe Lys Phe
85 90 95

Met Asn Asp Ser Thr Ile Tyr Lys Gly Gln Leu Gly Val Asn Asn Glu
100 105 110

Ile Leu Leu Thr Thr Tyr Leu Glu Thr Cys Gln Glu Asn Thr Glu
115 120 125

Tyr Tyr Phe Gln Ala Lys Thr Asp Met Tyr Ile Tyr Lys Asn Tyr Glu
130 135 140

His Leu Lys Thr Val Pro Leu Ser Ser Ile Thr Thr Leu Asp Thr Phe
145 150 155 160

Ile Ala Leu Asn Phe Thr Leu Leu Glu Asn Val Asp Phe Lys Val Ile
165 170 175

Glu Leu Tyr Thr Arg Asp Glu Lys Arg Leu Ser Asn Val Phe Asp Ile
180 185 190

Glu Thr Met
195

<210> 3
<211> 19
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<220>
<223> PCR amplification primer for pGHV-gpB gene sequences

<400> 3
mgaacaacgt yaaytgyga 19

<210> 4
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<220>
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<400> 4
mgaacaacgt yaaytgyct 19

<210> 5
<211> 17
<212> DNA
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<220>
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<400> 5
mgaacaacgt yaaytgy 17

<210> 6
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<220>
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<400> 6
cartcartwt gcmtaygac 19

<210> 7
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<220>
<221> misc_feature
<223> n=i

<400> 7
carntncart wtgcmtayg 19

<210> 8
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<400> 8
gtbatgwsha gvathtaygg 20

<210> 9
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<400> 9
gtbatgwshg cvathtaygg 20

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<400> 10
swcatnacrs tngtnggrtt 20

<210> 11
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<223> n=i

<400> 11
trngygtart arttrtaytc yctraa 26

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<220>
<223> PCR amplification primer for pGHV-gpB gene sequences

<400> 12
gtartarttr taytcyctra a 21

<210> 13
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<220>
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<400> 13
ctgraarttr taytcycgra a 21

<210> 14
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<220>
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<223> n=i

<400> 14
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<220>
<223> PCR amplification primer for Epstein-Barr Virus genome

<400> 15
agaactaccg tcaactgcct 20

<210> 16
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<212> DNA
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<220>
<223> PCR amplification primer for Epstein-Barr Virus genome

<400> 16
agaactaccg tcaactgc 18

<210> 17
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<400> 17
cagatccaat ttgcctacga c 21

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<400> 19
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<210> 20
<211> 20
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<400> 20
gacatgacgg tggttggatt 20

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<220>
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<400> 21
tgcgccctgga agttgtactc ccggaa 26

<210> 22
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<212> DNA
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<220>
<223> PCR amplification primer for Epstein-Barr Virus genome

<400> 22
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<210> 23
<211> 2598
<212> DNA
<213> artificial

<220>
<223> cDNA for porcine gamma herpesvirus gpB gene

<400> 23
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gcttttatt cacttagtat agcagagacc ggtgtaccc cacccaaa tacagcgacc 120
tggctactg aatccgcgt aacaggtcac tatgaaacac acgattcaag ccattggtaa 180
agaggaaaca acgaaaacag agattcagaa gagaaaaata aaaacattt tggatcgct 240
tctacgttc cttacagat atgcgtgcc tccggatgg gagatgtctt tagatttcag 300
accgaccatg tggcccga tgccagtgat atggacaca gtgaggggat tctactaatt 360
tacaaacaga acattattcc atttatgttt agagtttaga aatatagaaa agttgttaca 420
acaagtactg tctacaatgg tatttattct gactcttata ccaaccaaca tactttctat 480
aatcaatcg aaccttggga gacagaaaag atggacacaa tatatcagtg ttttaattct 540
ttaagactaa acacaggtgg aatctgttt acttatgttag atagagatga tataaataatg 600
acagtgttc tgcaacctgt tgacgggtgt acgcccgtg tgaagaggta tggcagtcaa 660
ccagagctgt accttgaacc tggctggtt tgggttagtt atagaagacg aactacagtg 720
aactgtgaac taatggacat gtttgcaga tcaaatcctc catttgattt ctttggtaca 780
gctacaggtg atacgggtgg aatgtctcca ttttggatgg gtgaagatga tcatggaaat 840
aagatgcacg agaagccatg gtttggtagt gtgataaata actacaaggt ggtggactat 900
caaaacagag ggactgtacc cttggaaaaa acaaggatat ttctagatag ggaagagtt 960
acattatctt gggaaaagca tctaaaaaat atgtcatatt gtccactaac attatggaaa 1020
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atcacagcg tattcacaac tagtaaagaa gacatgaaag agttcaatac gacatatacat 1140
tgcgtcaacg aggaataaaa ggcagaaaata gagaagaaat atgcaaaatg aaactcaact 1200
cactctaaat atggagatct gaaatactt aaaacagatg ggggtctcta tttgtctgg 1260
caaccttta ttcaaaacag gcttcttgc gctaagaaca aactgaacaa tgagacttat 1320
tccaggagat cacgacgtca ggcagaatct actactgacc caatgtggaa gatgactgg 1380
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tgcgtgagc agcatagagc tgctctggg tggatgagc tcagcaagat taatcccaca 1560
acgtcatga gcatgattt caatagaccc gtatcagcca aaagaatagg agatgtcatt 1620
tcagtctcta actgtattgt gtagaccaa accagtgtct cattacataa aagtctcagg 1680
cttctcagtg catcgatga aagtgcctc tctagacctc cagtgcatt taagttatg 1740
aatgacagta ctattacaa agggcaacta ggagtcaata atgagattct cttaccacaa 1800
acataccctt aaacatgtca ggaaaacact gaggattact ttcaggcaaa gacagacatg 1860
tacatttaca aaaactatga gcatttgcag actgtgcctt tatcttcgtat caccacacta 1920
gatacatata tagcccttaa ttttacacta ttggagaatg ttgactttaa agtcattgaa 1980
cttataccca gggacagaaa gaggcttagt aatgtcttg acattgaaac aatgtttagg 2040
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atgttaaaca ctttataa 2598

<210> 24
<211> 865
<212> PRT
<213> artificial

<220>
<223> Deduced amino acid sequence of porcine gamma herpesvirus gpB gene

<400> 24
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1 5 10 15

Leu Tyr Gln Val Ala Leu Tyr Ser Leu Ser Ile Ala Glu Thr Gly Val
20 25 30

Thr Ser Pro Pro Asn Thr Ala Thr Trp Ser Thr Glu Ser Pro Leu Thr
35 40 45

Gly His Tyr Gly Thr His Asp Ser Ser His Gly Glu Arg Gly Asn Asn
50 55 60

Glu Asn Arg Asp Ser Glu Glu Gln Asn Lys Asn Ile Tyr Gly Ser Pro
65 70 75 80

Ser Thr Phe Pro Tyr Arg Val Cys Ser Ala Ser Gly Val Gly Asp Val
85 90 95

Phe Arg Phe Gln Thr Asp His Val Cys Pro Asp Ala Ser Asp Met Val
100 105 110

His Ser Glu Gly Ile Leu Leu Ile Tyr Lys Gln Asn Ile Ile Pro Phe
115 120 125

Met Phe Arg Val Arg Lys Tyr Arg Lys Val Val Thr Thr Ser Thr Val
130 135 140

Tyr Asn Gly Ile Tyr Ser Asp Ser Ile Thr Asn Gln His Thr Phe Tyr
145 150 155 160

Lys Ser Ile Glu Pro Trp Glu Thr Glu Lys Met Asp Thr Ile Tyr Gln
165 170 175

Cys Phe Asn Ser Leu Arg Leu Asn Thr Gly Gly Asn Leu Leu Thr Tyr
180 185 190

Val Asp Arg Asp Asp Ile Asn Met Thr Val Phe Leu Gln Pro Val Asp
195 200 205

Gly Val Thr Pro Asp Val Lys Arg Tyr Gly Ser Gln Pro Glu Leu Tyr
210 215 220

Leu Glu Pro Gly Trp Phe Trp Gly Ser Tyr Arg Arg Arg Thr Thr Val
225 230 235 240

Asn Cys Glu Leu Met Asp Met Phe Ala Arg Ser Asn Pro Pro Phe Asp
245 250 255

Phe Phe Val Thr Ala Thr Gly Asp Thr Val Glu Met Ser Pro Phe Trp
 260 265 270

 Ser Gly Glu Asp Asp His Glu Asn Lys Met His Glu Lys Pro Trp Phe
 275 280 285

 Val Ser Val Ile Asn Asn Tyr Lys Val Val Asp Tyr Gln Asn Arg Gly
 290 295 300

 Thr Val Pro Leu Gly Lys Thr Arg Ile Phe Leu Asp Arg Glu Glu Tyr
 305 310 315 320

 Thr Leu Ser Trp Glu Lys His Leu Lys Asn Met Ser Tyr Cys Pro Leu
 325 330 335

 Thr Leu Trp Lys Ala Phe Tyr Asn Gly Ile Gln Thr Glu His Ser Gly
 340 345 350

 Ser Tyr His Phe Val Ala Asn Asp Ile Thr Ala Ser Phe Thr Thr Ser
 355 360 365

 Lys Glu Asp Met Lys Glu Phe Asn Thr Thr Tyr His Cys Leu Asn Glu
 370 375 380

 Glu Ile Lys Ala Glu Ile Glu Lys Lys Tyr Ala Lys Val Asn Ser Thr
 385 390 395 400

 His Ser Lys Tyr Gly Asp Leu Lys Tyr Phe Lys Thr Asp Gly Gly Leu
 405 410 415

 Tyr Leu Val Trp Gln Pro Leu Ile Gln Asn Arg Leu Leu Asp Ala Lys
 420 425 430

 Asn Lys Leu Asn Asn Glu Thr Tyr Ser Arg Arg Ser Arg Arg Gln Ala
 435 440 445

 Glu Ser Thr Thr Asp Pro Met Met Glu Met Thr Gly Asn Gly Ala Gly
 450 455 460

 Gly Glu Tyr Ser Ser Glu Asn Ser Ile Thr Val Ala Gln Val Gln Tyr
 465 470 475 480

 Ala Tyr Asp Asn Leu Arg Ile Arg Ile Asn Asn Ile Leu Glu Asp Leu
 485 490 495

 Ser Lys Ala Trp Cys Arg Glu Gln His Arg Ala Ala Leu Val Trp Asn
 500 505 510

 Glu Leu Ser Lys Ile Asn Pro Thr Ser Val Met Ser Met Ile Tyr Asn
 515 520 525

 Arg Pro Val Ser Ala Lys Arg Ile Gly Asp Val Ile Ser Val Ser Asn
 530 535 540

 Cys Ile Val Val Asp Gln Thr Ser Val Ser Leu His Lys Ser Leu Arg
 545 550 555 560

Leu	Leu	Ser	Ala	Ser	Asp	Glu	Lys	Cys	Phe	Ser	Arg	Pro	Pro	Val	Thr		
														565	570	575	
Phe	Lys	Phe	Met	Asn	Asp	Ser	Thr	Ile	Tyr	Lys	Gly	Gln	Leu	Gly	Val		
														580	585	590	
Asn	Asn	Glu	Ile	Leu	Leu	Thr	Thr	Thr	Tyr	Leu	Glu	Thr	Cys	Gln	Glu		
														595	600	605	
Asn	Thr	Glu	Tyr	Tyr	Phe	Gln	Ala	Lys	Thr	Asp	Met	Tyr	Ile	Tyr	Lys		
														610	615	620	
Asn	Tyr	Glu	His	Leu	Lys	Thr	Val	Pro	Leu	Ser	Ser	Ile	Thr	Thr	Leu		
														625	630	635	640
Asp	Thr	Phe	Ile	Ala	Leu	Asn	Phe	Thr	Leu	Leu	Glu	Asn	Val	Asp	Phe		
														645	650	655	
Lys	Val	Ile	Glu	Leu	Tyr	Thr	Arg	Asp	Glu	Lys	Arg	Leu	Ser	Asn	Val		
														660	665	670	
Phe	Asp	Ile	Glu	Thr	Met	Phe	Arg	Glu	Tyr	Asn	Tyr	Tyr	Ala	Gln	Arg		
														675	680	685	
Val	Ser	Gly	Leu	Arg	Lys	Asp	Leu	Leu	Asp	Leu	Ser	Thr	Asn	Arg	Asn		
														690	695	700	
Gln	Phe	Val	Asp	Ala	Phe	Gly	Ser	Leu	Met	Asp	Asp	Leu	Gly	Ala	Val		
														705	710	715	720
Gly	Gln	Thr	Val	Val	Asn	Ala	Val	Ser	Gly	Val	Ala	Thr	Leu	Phe	Ser		
														725	730	735	
Ser	Ile	Val	Thr	Gly	Phe	Ile	Asn	Phe	Ile	Lys	Asn	Pro	Phe	Gly	Gly		
														740	745	750	
Met	Leu	Met	Ile	Ile	Val	Val	Ile	Gly	Val	Leu	Phe	Ala	Ile	Tyr	Phe		
														755	760	765	
Leu	Thr	Lys	Lys	Thr	Lys	Ile	Tyr	Glu	Thr	Ala	Pro	Ile	Lys	Met	Ile		
														770	775	780	
Tyr	Pro	Glu	Ile	Asp	Lys	Leu	Lys	Glu	Arg	Glu	Gly	Lys	Ser	Glu	Ile		
														785	790	795	800
Ala	Pro	Ile	Ser	Glu	Glu	Leu	Glu	Arg	Ile	Val	Leu	Ala	Met	His			
														805	810	815	
Ile	His	Gln	Gln	Asn	Ser	His	Met	Glu	Thr	Lys	Thr	Arg	Lys	Asp	Pro		
														820	825	830	
Lys	Asp	Ser	Ile	Leu	Thr	Arg	Ala	Gln	Asn	Met	Leu	Arg	Lys	Arg	Ser		
														835	840	845	
Gly	Tyr	Ser	Asn	Leu	Lys	Asn	Ala	Glu	Ser	Val	Glu	Met	Leu	Asn	Thr		
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Leu
865

<210> 25
<211> 24
<212> DNA
<213> artificial

<220>
<223> Sequencing primer for TOPO-pCRII: bases 434-458

<400> 25
cgccagggtt ttcccagtca cgac 24

<210> 26
<211> 17
<212> DNA
<213> artificial

<220>
<223> M13 reverse sequencing primer for TOPO-pCRII: bases 205-222

<400> 26
caggaaacag ctatgac 17

<210> 27
<211> 20
<212> DNA
<213> artificial

<220>
<223> Sequencing primer for porcine gamma herpesvirus gpB gene: bases 1989-2008

<400> 27
cagggacgag aagaggctta 20

<210> 28
<211> 19
<212> DNA
<213> artificial

<220>
<223> Sequencing primer for porcine gamma herpesvirus gpB gene: bases 1513-1531

<400> 28
acaccagagc agctctatg 19

<210> 29
<211> 24
<212> DNA
<213> artificial

<220>
<223> Sequencing primer for porcine gamma herpesvirus gpB gene: bases
2399-2422

<400> 29
tagcaccaat cagtgaagaa gagc 24

<210> 30
<211> 22
<212> DNA
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<220>
<223> Sequencing primer for porcine gamma herpesvirus gpB gene: bases
322-343

<400> 30
gccagtgata tggcacacag tg 22

<210> 31
<211> 24
<212> DNA
<213> artificial

<220>
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140-163

<400> 31
taacagggtca ctatgaaaca cacg 24

<210> 32
<211> 24
<212> DNA
<213> artificial

<220>
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537-560

<400> 32
ttctttaaga ctaaacacacag gtgg 24

<210> 33
<211> 21
<212> DNA
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<220>
<223> Sequencing primer for porcine gamma herpesvirus gpB gene: bases
815-835

<400> 33

ggagtggtga agatgatcat g

21

<210> 34
<211> 25
<212> DNA
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<220>
<223> Sequencing primer for porcine gamma herpesvirus gpB gene: bases
993-1017

<400> 34
ccataatgtt agtggacaat atgac

25

<210> 35
<211> 21
<212> DNA
<213> artificial

<220>
<223> Sequencing primer for porcine gamma herpesvirus gpB gene: bases
1073-1093

<400> 35
atgacgctgt gatgtcattg g

21

<210> 36
<211> 22
<212> DNA
<213> artificial

<220>
<223> Sequencing primer for porcine gamma herpesvirus gpB gene: bases
1673-1694

<400> 36
gatgcactga gaagcctgag ac

22

<210> 37
<211> 823
<212> PRT
<213> Human herpesvirus 8

<400> 37
Met Thr Pro Arg Ser Arg Leu Ala Thr Leu Gly Thr Val Ile Leu Leu
1 5 10 15

Val Cys Phe Cys Ala Gly Ala Ala His Ser Arg Gly Asp Thr Phe Gln
20 25 30

Thr Ser Ser Ser Pro Thr Pro Pro Gly Ser Ser Ser Lys Ala Pro Thr
35 40 45

Lys	Pro	Gly	Glu	Glu	Ala	Ser	Gly	Pro	Lys	Ser	Val	Asp	Phe	Tyr	Gln
50															
														60	
Phe	Arg	Val	Cys	Ser	Ala	Ser	Ile	Thr	Gly	Glu	Leu	Phe	Arg	Phe	Asn
65															80
Leu	Glu	Gln	Thr	Cys	Pro	Asp	Thr	Lys	Asp	Lys	Tyr	His	Gln	Glu	Gly
															95
Ile	Leu	Leu	Val	Tyr	Lys	Lys	Asn	Ile	Val	Pro	His	Ile	Phe	Lys	Val
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Arg	Arg	Tyr	Arg	Lys	Ile	Ala	Thr	Ser	Val	Thr	Val	Tyr	Arg	Gly	Leu
															125
Thr	Glu	Ser	Ala	Ile	Thr	Asn	Lys	Tyr	Glu	Leu	Pro	Arg	Pro	Val	Pro
															140
Leu	Tyr	Glu	Ile	Ser	His	Met	Asp	Ser	Thr	Tyr	Gln	Cys	Phe	Ser	Ser
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Met	Lys	Val	Asn	Val	Asn	Gly	Val	Glu	Asn	Thr	Phe	Thr	Asp	Arg	Asp
															175
Asp	Val	Asn	Thr	Thr	Val	Phe	Leu	Gln	Pro	Val	Glu	Gly	Leu	Thr	Asp
															190
Asn	Ile	Gln	Arg	Tyr	Phe	Ser	Gln	Pro	Val	Ile	Tyr	Ala	Glu	Pro	Gly
															205
Trp	Phe	Pro	Gly	Ile	Tyr	Arg	Val	Arg	Thr	Thr	Val	Asn	Cys	Glu	Ile
															220
Val	Asp	Met	Ile	Ala	Arg	Ser	Ala	Glu	Pro	Tyr	Asn	Tyr	Phe	Val	Thr
															240
Ser	Leu	Gly	Asp	Thr	Val	Glu	Val	Ser	Pro	Phe	Cys	Tyr	Asn	Glu	Ser
															255
Ser	Cys	Ser	Thr	Thr	Pro	Ser	Asn	Lys	Asn	Gly	Leu	Ser	Val	Gln	Val
															270
Val	Leu	Asn	His	Thr	Val	Val	Thr	Tyr	Ser	Asp	Arg	Gly	Thr	Ser	Pro
															285
Thr	Pro	Gln	Asn	Arg	Ile	Phe	Val	Glu	Thr	Gly	Ala	Tyr	Thr	Leu	Ser
															300
Trp	Ala	Ser	Glu	Ser	Lys	Thr	Thr	Ala	Val	Cys	Pro	Leu	Ala	Leu	Trp
															320
Lys	Thr	Phe	Pro	Arg	Ser	Ile	Gln	Thr	Thr	His	Glu	Asp	Ser	Phe	His
															335
Phe	Val	Ala	Asn	Glu	Ile	Thr	Ala	Thr	Phe	Thr	Ala	Pro	Leu	Thr	Pro
															350

Val Ala Asn Phe Thr Asp Thr Tyr Ser Cys Leu Thr Ser Asp Ile Asn
 355 360 365
 Thr Thr Leu Asn Ala Ser Lys Ala Lys Leu Ala Ser Thr His Val Pro
 370 375 380
 Asn Gly Thr Val Gln Tyr Phe His Thr Thr Gly Gly Leu Tyr Leu Val
 385 390 395 400
 Trp Gln Pro Met Ser Ala Ile Asn Leu Thr His Ala Gln Gly Asp Ser
 405 410 415
 Gly Asn Pro Thr Ser Ser Pro Pro Pro Ser Ala Ser Pro Met Thr Thr
 420 425 430
 Ser Ala Ser Arg Arg Lys Arg Arg Ser Ala Ser Thr Ala Ala Ala Gly
 435 440 445
 Gly Gly Gly Ser Thr Asp Asn Leu Ser Tyr Thr Gln Leu Gln Phe Ala
 450 455 460
 Tyr Asp Lys Leu Arg Asp Gly Ile Asn Gln Val Leu Glu Glu Leu Ser
 465 470 475 480
 Arg Ala Trp Cys Arg Glu Gln Val Arg Asp Asn Leu Met Trp Tyr Glu
 485 490 495
 Leu Ser Lys Ile Asn Pro Thr Ser Val Met Thr Ala Ile Tyr Gly Arg
 500 505 510
 Pro Val Ser Ala Lys Phe Val Gly Asp Ala Ile Ser Val Thr Glu Cys
 515 520 525
 Ile Asn Val Asp Gln Ser Ser Val Asn Ile His Lys Ser Leu Arg Thr
 530 535 540
 Asn Ser Lys Asp Val Cys Tyr Ala Arg Pro Leu Val Thr Phe Lys Phe
 545 550 555 560
 Leu Asn Ser Ser Asn Leu Phe Thr Gly Gln Leu Gly Ala Arg Asn Glu
 565 570 575
 Ile Ile Leu Thr Asn Asn Gln Val Glu Thr Cys Lys Asp Thr Cys Glu
 580 585 590
 His Tyr Phe Ile Thr Arg Asn Glu Thr Leu Val Tyr Lys Asp Tyr Ala
 595 600 605
 Tyr Leu Arg Thr Ile Asn Thr Thr Asp Ile Ser Thr Leu Asn Thr Phe
 610 615 620
 Ile Ala Leu Asn Leu Ser Phe Ile Gln Asn Ile Asp Phe Lys Ala Ile
 625 630 635 640
 Glu Leu Tyr Ser Ser Ala Glu Lys Arg Leu Ala Ser Ser Val Phe Asp
 645 650 655

Leu Glu Thr Met Phe Arg Glu Tyr Asn Tyr Tyr Thr His Arg Leu Ala
660 665 670

Gly Leu Arg Glu Asp Leu Asp Asn Thr Ile Asp Met Asn Lys Glu Arg
675 680 685

Phe Val Arg Asp Leu Ser Glu Ile Val Ala Asp Leu Gly Gly Ile Gly
690 695 700

Lys Thr Val Val Asn Val Ala Ser Ser Val Val Thr Leu Cys Gly Ser
705 710 715 720

Leu Val Thr Gly Phe Ile Asn Phe Ile Lys His Pro Leu Gly Gly Met
725 730 735

Leu Met Ile Ile Ile Val Ile Ala Ile Ile Leu Ile Ile Phe Met Leu
740 745 750

Ser Arg Arg Thr Asn Thr Ile Ala Gln Ala Pro Val Lys Met Ile Tyr
755 760 765

Pro Asp Val Asp Arg Arg Ala Pro Pro Ser Gly Gly Ala Pro Thr Arg
770 775 780

Glu Glu Ile Lys Asn Ile Leu Leu Gly Met His Gln Leu Gln Gln Glu
785 790 795 800

Arg Gln Lys Ala Asp Asp Leu Lys Lys Ser Thr Pro Ser Val Phe Gln
805 810 815

Arg Thr Ala Asn Gly Leu Arg
820

<210> 38
<211> 808
<212> PRT
<213> Rhesus monkey rhadinovirus

<400> 38
Met Met Ile Thr Asn Arg Thr Arg Arg Leu Leu Arg Ala Trp Val Val
1 5 10 15

Ile Ile Ala Ile Gly Thr Ala Val Gly Glu Asn Val Thr Thr Pro Lys
20 25 30

Gly Ala Thr Thr Ala Lys Pro Thr Pro Gly Pro Ser Thr Pro Thr
35 40 45

Pro Pro Glu Asn Pro Pro Arg Ala Glu Ala Phe Lys Phe Arg Val Cys
50 55 60

Ser Ala Ser Ala Thr Gly Glu Leu Phe Arg Phe Asn Leu Glu Lys Thr
65 70 75 80

Cys Pro Gly Thr Glu Asp Lys Thr His Gln Glu Gly Ile Leu Met Val
85 90 95

Phe Lys Lys Asn Ile Val Pro His Ile Phe Lys Val Arg Arg Tyr Arg
100 105 110

Lys Val Ala Thr Ser Val Thr Val Tyr Arg Gly Trp Thr Glu Thr Ala
115 120 125

Val Thr Gly Lys Gln Glu Val Ile Arg Pro Val Pro Gln Tyr Glu Ile
130 135 140

Asn His Met Asp Thr Thr Tyr Gln Cys Phe Ser Ser Met Arg Val Asn
145 150 155 160

Val Asn Gly Ile Val Asn Thr Tyr Thr Asp Arg Asp Phe Thr Asn Gln
165 170 175

Thr Val Phe Leu Gln Pro Val Glu Gly Leu Thr Asp Asn Ile Gln Arg
180 185 190

Tyr Phe Ser Gln Pro Val Leu Tyr Thr Pro Gly Trp Phe Pro Gly
195 200 205

Ile Tyr Arg Val Arg Thr Thr Val Asn Cys Glu Ile Val Asp Met Ile
210 215 220

Ala Arg Ser Ala Glu Pro Tyr Ser Tyr Phe Val Thr Ala Leu Gly Asp
225 230 235 240

Thr Val Glu Val Ser Pro Phe Cys His Asn Asp Ser Thr Cys Ser Val
245 250 255

Ala Glu Lys Thr Glu Asn Gly Leu Gly Ala Arg Val Leu Thr Asn Tyr
260 265 270

Thr Met Val Asp Phe Ala Thr Arg Ala Pro Thr Thr Glu Thr Arg Val
275 280 285

Phe Ala Asp Ser Gly Glu Tyr Thr Val Ser Trp Lys Ala Glu Asp Pro
290 295 300

Lys Ser Ala Val Cys Ala Leu Thr Leu Trp Lys Thr Phe Pro Arg Ala
305 310 315 320

Ile Gln Thr Thr His Glu Ala Ser Tyr His Phe Val Ala Asn Asp Val
325 330 335

Thr Ala Thr Phe Thr Ser Pro Leu Ser Glu Val Ala Asn Phe Thr Gly
340 345 350

Thr Tyr Ser Cys Leu Asp Glu Val Ile Gln Lys Thr Leu Asn Asp Thr
355 360 365

Ile Lys Lys Leu Ser Asp Thr His Val Thr Asn Gly Ser Ala Gln Tyr
370 375 380

Tyr Lys Thr Glu Gly Gly Leu Phe Leu Leu Trp Gln Pro Leu Thr Pro
385 390 395 400

Leu Ser Leu Val Asp Glu Met Arg Gly Leu Asn Gly Thr Thr Pro Ala
 405 410 415
 Pro Pro Ala Thr Thr Ser Thr Val Ser Arg Val Arg Arg Ser Val Asn
 420 425 430
 Thr Asn Glu Gln Ala Thr Asp Asn Leu Ala Ala Pro Gln Leu Gln Phe
 435 440 445
 Ala Tyr Asp Lys Leu Arg Ala Ser Ile Asn Lys Val Leu Glu Glu Leu
 450 455 460
 Ser Arg Ala Trp Cys Arg Glu Gln Val Arg Asp Thr Tyr Met Trp Tyr
 465 470 475 480
 Glu Leu Ser Lys Ile Asn Pro Thr Ser Val Met Thr Ala Ile Tyr Gly
 485 490 495
 Arg Pro Val Ser Ala Lys Phe Val Gly Asp Ala Ile Ser Val Thr Asp
 500 505 510
 Cys Val Ala Val Asp Gln Ala Ser Val Ser Ile His Lys Ser Leu Arg
 515 520 525
 Thr Ser Thr Pro Gly Met Cys Tyr Ser Arg Pro Pro Val Thr Phe Arg
 530 535 540
 Phe Leu Asn Ser Thr Thr Leu Phe Lys Gly Gln Leu Gly Pro Arg Asn
 545 550 555 560
 Glu Ile Ile Leu Thr Asp Asn Gln Val Glu Ala Cys Lys Glu Thr Cys
 565 570 575
 Glu His Tyr Phe Ile Ala Ser Asn Val Thr Tyr Tyr Lys Asp Tyr
 580 585 590
 Val Phe Val Lys Lys Ile Asn Thr Ser Glu Ile Ser Thr Leu Gly Thr
 595 600 605
 Phe Ile Ala Leu Asn Leu Ser Phe Ile Glu Asn Ile Asp Phe Arg Val
 610 615 620
 Ile Glu Leu Tyr Ser Arg Ala Glu Lys Lys Leu Ser Gly Ser Val Phe
 625 630 635 640
 Asp Ile Glu Thr Met Phe Arg Glu Tyr Asn Tyr Tyr Thr Gln Arg Leu
 645 650 655
 Ala Gly Leu Arg Glu Asp Leu Asp Asn Thr Ile Asp Leu Asn Arg Asp
 660 665 670
 Arg Leu Ala Arg Asp Leu Ser Glu Ile Val Ala Asp Leu Gly Asp Val
 675 680 685
 Gly Arg Thr Val Val Asn Val Ala Ser Ser Val Ile Thr Leu Phe Gly
 690 695 700

Ser Ile Val Ser Gly Phe Ile Asn Phe Ile Lys Ser Pro Phe Gly Gly
705 710 715 720

Met Leu Met Ile Leu Val Ile Val Ala Val Val Leu Ile Val Phe Ala
725 730 735

Leu Asn Arg Arg Thr Asn Ala Ile Ala Gln Ala Pro Ile Arg Met Ile
740 745 750

Tyr Pro Asp Ile Asp Lys Met Gln Pro Ser Gly Gly Lys Val Asp Gln
755 760 765

Glu Gln Ile Lys Asn Ile Leu Ala Gly Met His Gln Leu Gln Gln Glu
770 775 780

Glu Arg Arg Arg Leu Asp Glu Gln Gln Arg Ser Ala Pro Ser Leu Phe
785 790 795 800

Arg Arg Ala Ser Asp Gly Leu Lys
805

<210> 39

<211> 831

<212> PRT

<213> Murine herpesvirus 68

<400> 39

Met Tyr Pro Thr Val Lys Ser Met Arg Val Ala His Leu Thr Asn Leu
1 5 10 15

Leu Thr Leu Leu Cys Leu Leu Cys His Thr His Leu Tyr Val Cys Gln
20 25 30

Pro Thr Thr Leu Arg Gln Pro Ser Asp Met Thr Pro Ala Gln Asp Ala
35 40 45

Pro Thr Glu Thr Pro Pro Pro Leu Ser Thr Asn Thr Asn Arg Gly Phe
50 55 60

Glu Tyr Phe Arg Val Cys Gly Val Ala Ala Thr Gly Glu Thr Phe Arg
65 70 75 80

Phe Asp Leu Asp Lys Thr Cys Pro Ser Thr Gln Asp Lys Lys His Val
85 90 95

Glu Gly Ile Leu Leu Val Tyr Lys Ile Asn Ile Val Pro Tyr Ile Phe
100 105 110

Lys Ile Arg Arg Tyr Arg Lys Ile Ile Thr Gln Leu Thr Ile Trp Arg
115 120 125

Gly Leu Thr Thr Ser Ser Val Thr Gly Lys Phe Glu Met Ala Thr Gln
130 135 140

Ala His Glu Trp Glu Val Gly Asp Phe Asp Ser Ile Tyr Gln Cys Tyr
145 150 155 160

Asn Ser Ala Thr Met Val Val Asn Asn Val Arg Gln Val Tyr Val Asp
 165 170 175

 Arg Asp Gly Val Asn Lys Thr Val Asn Ile Arg Pro Val Asp Gly Leu
 180 185 190

 Thr Gly Asn Ile Gln Arg Tyr Phe Ser Gln Pro Thr Leu Tyr Ser Glu
 195 200 205

 Pro Gly Trp Met Pro Gly Phe Tyr Arg Val Arg Thr Thr Val Asn Cys
 210 215 220

 Glu Ile Val Asp Met Val Ala Arg Ser Met Asp Pro Tyr Asn Tyr Ile
 225 230 235 240

 Ala Thr Ala Leu Gly Asp Ser Leu Glu Leu Ser Pro Phe Gln Thr Phe
 245 250 255

 Asp Asn Thr Ser Gln Ser Thr Ala Pro Lys Arg Ala Asp Met Arg Val
 260 265 270

 Arg Glu Val Lys Asn Tyr Lys Phe Val Asp Tyr Asn Asn Arg Gly Thr
 275 280 285

 Ala Pro Ala Gly Gln Ser Arg Thr Phe Leu Glu Thr Pro Ser Ala Thr
 290 295 300

 Tyr Ser Trp Lys Thr Ala Thr Arg Gln Thr Ala Thr Cys Asp Leu Val
 305 310 315 320

 His Trp Lys Thr Phe Pro Arg Ala Ile Gln Thr Ala His Glu His Ser
 325 330 335

 Tyr His Phe Val Ala Asn Glu Val Thr Ala Thr Phe Asn Thr Pro Leu
 340 345 350

 Thr Glu Val Glu Asn Phe Thr Ser Thr Tyr Ser Cys Val Ser Asp Gln
 355 360 365

 Ile Asn Lys Thr Ile Ser Glu Tyr Ile Gln Lys Leu Asn Asn Ser Tyr
 370 375 380

 Val Ala Ser Gly Lys Thr Gln Tyr Phe Lys Thr Asp Gly Asn Leu Tyr
 385 390 395 400

 Leu Ile Trp Gln Pro Leu Glu His Pro Glu Ile Glu Asp Ile Asp Glu
 405 410 415

 Asp Ser Asp Pro Glu Pro Thr Pro Ala Pro Pro Lys Ser Thr Arg Arg
 420 425 430

 Lys Arg Glu Ala Ala Asp Asn Gly Asn Ser Thr Ser Glu Val Ser Lys
 435 440 445

 Gly Ser Glu Asn Pro Leu Ile Thr Ala Gln Ile Gln Phe Ala Tyr Asp
 450 455 460

Lys Leu Thr Thr Ser Val Asn Asn Val Leu Glu Glu Leu Ser Arg Ala
 465 470 475 480
 Trp Cys Arg Glu Gln Val Arg Asp Thr Leu Met Trp Tyr Glu Leu Ser
 485 490 495
 Lys Val Asn Pro Thr Ser Val Met Ser Ala Ile Tyr Gly Lys Pro Val
 500 505 510
 Ala Ala Arg Tyr Val Gly Asp Ala Ile Ser Val Thr Asp Cys Ile Tyr
 515 520 525
 Val Asp Gln Ser Ser Val Asn Ile His Gln Ser Leu Arg Leu Gln His
 530 535 540
 Asp Lys Thr Thr Cys Tyr Ser Arg Pro Arg Val Thr Phe Lys Phe Ile
 545 550 555 560
 Asn Ser Thr Asp Pro Leu Thr Gly Gln Leu Gly Pro Arg Lys Glu Ile
 565 570 575
 Ile Leu Ser Asn Thr Asn Ile Glu Thr Cys Lys Asp Glu Ser Glu His
 580 585 590
 Tyr Phe Ile Val Gly Glu Tyr Ile Tyr Tyr Tyr Lys Asn Tyr Ile Phe
 595 600 605
 Glu Glu Lys Leu Asn Leu Ser Ser Ile Ala Thr Leu Asp Thr Phe Ile
 610 615 620
 Ala Leu Asn Ile Ser Phe Ile Glu Asn Ile Asp Phe Lys Thr Val Glu
 625 630 635 640
 Leu Tyr Ser Ser Thr Glu Arg Lys Leu Ala Ser Ser Val Phe Asp Ile
 645 650 655
 Glu Ser Met Phe Arg Glu Tyr Asn Tyr Tyr Thr Tyr Ser Leu Ala Gly
 660 665 670
 Ile Lys Lys Asp Leu Asp Asn Thr Ile Asp Tyr Asn Arg Asp Arg Leu
 675 680 685
 Val Gln Asp Leu Ser Asp Met Met Ala Asp Leu Gly Asp Ile Gly Arg
 690 695 700
 Ser Val Val Asn Val Val Ser Ser Val Val Thr Phe Phe Ser Ser Ile
 705 710 715 720
 Val Thr Gly Phe Ile Lys Phe Phe Thr Asn Pro Leu Gly Gly Ile Phe
 725 730 735
 Ile Leu Leu Ile Ile Gly Gly Ile Ile Phe Leu Val Val Val Leu Asn
 740 745 750
 Arg Arg Asn Ser Gln Phe His Asp Ala Pro Ile Lys Met Leu Tyr Pro
 755 760 765

Ser Val Glu Asn Tyr Ala Ala Arg Gln Ala Pro Pro Pro Tyr Ser Ala
 770 775 780
 Ser Pro Pro Ala Ile Asp Lys Glu Glu Ile Lys Arg Ile Leu Leu Gly
 785 790 795 800
 Met His Gln Val His Gln Glu Glu Lys Glu Ala Gln Lys Gln Leu Thr
 805 810 815
 Asn Ser Gly Pro Thr Leu Trp Gln Lys Ala Thr Gly Phe Leu Arg
 820 825 830
 <210> 40
 <211> 844
 <212> PRT
 <213> Bovine herpesvirus 4
 <400> 40
 Tyr Tyr Lys Thr Ile Leu Phe Phe Ala Leu Ile Lys Val Cys Ser Phe
 1 5 10 15
 Asn Gln Thr Thr His Ser Thr Thr Ser Pro Ser Ile Ser Ser
 20 25 30
 Thr Thr Ser Ser Thr Thr Ser Thr Ser Lys Pro Ser Asn Thr Thr
 35 40 45
 Ser Thr Asn Ser Ser Leu Ala Ala Ser Pro Gln Asn Thr Ser Thr Ser
 50 55 60
 Lys Pro Ser Thr Asp Asn Gln Gly Thr Ser Thr Pro Thr Ile Pro Thr
 65 70 75 80
 Val Thr Asp Asp Thr Ala Ser Lys Asn Phe Tyr Lys Tyr Arg Val Cys
 85 90 95
 Ser Ala Ser Ser Ser Gly Glu Leu Phe Arg Phe Asp Leu Asp Gln
 100 105 110
 Thr Cys Pro Asp Thr Lys Asp Lys Lys His Val Glu Gly Ile Leu Leu
 115 120 125
 Val Leu Lys Lys Asn Ile Val Pro Tyr Ile Phe Lys Val Arg Lys Tyr
 130 135 140
 Arg Lys Ile Ala Thr Ser Val Thr Val Tyr Arg Gly Trp Ser Gln Ala
 145 150 155 160
 Ala Val Thr Asn Arg Asp Asp Ile Ser Arg Ala Ile Pro Tyr Asn Glu
 165 170 175
 Ile Ser Met Ile Asp Arg Thr Tyr His Cys Phe Ser Ala Met Ala Thr
 180 185 190
 Val Ile Asn Gly Ile Leu Asn Thr Tyr Ile Asp Arg Asp Ser Glu Asn
 195 200 205

Lys	Ser	Val	Pro	Leu	Gln	Pro	Val	Ala	Gly	Leu	Thr	Glu	Asn	Ile	Asn
210						215						220			
Arg	Tyr	Phe	Ser	Gln	Pro	Leu	Ile	Tyr	Ala	Glu	Pro	Gly	Trp	Phe	Pro
225						230						235			240
Gly	Ile	Tyr	Arg	Val	Arg	Thr	Thr	Val	Asn	Cys	Glu	Val	Val	Asp	Met
						245						250			255
Tyr	Ala	Arg	Ser	Val	Glu	Pro	Tyr	Thr	His	Phe	Ile	Thr	Ala	Leu	Gly
						260						265			270
Asp	Thr	Ile	Glu	Ile	Ser	Pro	Phe	Cys	His	Asn	Asn	Ser	Gln	Cys	Thr
						275						280			285
Thr	Gly	Asn	Ser	Thr	Ser	Arg	Asp	Ala	Thr	Lys	Val	Trp	Ile	Glu	Glu
						290						295			300
Asn	His	Gln	Thr	Val	Asp	Tyr	Glu	Arg	Arg	Gly	His	Pro	Thr	Lys	Asp
						305						310			320
Lys	Arg	Ile	Phe	Leu	Lys	Asp	Glu	Glu	Tyr	Thr	Ile	Ser	Trp	Lys	Ala
						325						330			335
Glu	Asp	Arg	Glu	Arg	Ala	Ile	Cys	Asp	Phe	Val	Ile	Trp	Lys	Thr	Phe
						340						345			350
Pro	Arg	Ala	Ile	Gln	Thr	Ile	His	Asn	Glu	Ser	Phe	His	Phe	Val	Ala
						355						360			365
Asn	Glu	Val	Thr	Ala	Ser	Phe	Leu	Thr	Ser	Asn	Gln	Glu	Glu	Thr	Glu
						370						375			380
Leu	Arg	Gly	Asn	Thr	Glu	Ile	Leu	Asn	Cys	Met	Asn	Ser	Thr	Ile	Asn
						385						390			400
Glu	Thr	Leu	Glu	Glu	Thr	Val	Lys	Lys	Phe	Asn	Lys	Ser	His	Ile	Arg
						405						410			415
Asp	Gly	Glu	Val	Lys	Tyr	Tyr	Lys	Thr	Asn	Gly	Gly	Leu	Phe	Leu	Ile
						420						425			430
Trp	Gln	Ala	Met	Lys	Pro	Leu	Asn	Leu	Ser	Glu	His	Thr	Asn	Tyr	Thr
						435						440			445
Ile	Glu	Arg	Asn	Asn	Lys	Thr	Gly	Asn	Lys	Ser	Arg	Gln	Lys	Arg	Ser
						450						455			460
Val	Asp	Thr	Lys	Thr	Phe	Gln	Gly	Ala	Lys	Gly	Leu	Ser	Thr	Ala	Gln
						465						470			480
Val	Gln	Tyr	Ala	Tyr	Asp	His	Leu	Arg	Thr	Ser	Met	Asn	His	Ile	Leu
						485						490			495
Glu	Glu	Leu	Thr	Lys	Thr	Trp	Cys	Arg	Glu	Gln	Lys	Lys	Asp	Asn	Leu
						500						505			510

Met Trp Tyr Glu Leu Ser Lys Ile Asn Pro Val Ser Val Met Ala Ala
515 520 525

Ile Tyr Gly Lys Pro Val Ala Val Lys Ala Met Gly Asp Ala Phe Met
530 535 540

Val Ser Glu Cys Ile Asn Val Asp Gln Ala Ser Val Asn Ile His Lys
545 550 555 560

Ser Met Arg Thr Asp Asp Pro Lys Val Cys Tyr Ser Arg Pro Leu Val
565 570 575

Thr Phe Lys Phe Val Asn Ser Thr Ala Thr Phe Arg Gly Gln Leu Gly
580 585 590

Thr Arg Asn Glu Ile Leu Leu Thr Asn Thr His Val Glu Thr Cys Arg
595 600 605

Pro Thr Ala Asp His Tyr Phe Phe Val Lys Asn Met Thr His Tyr Phe
610 615 620

Lys Asp Tyr Lys Phe Val Lys Thr Met Asp Thr Asn Asn Ile Ser Thr
625 630 635 640

Leu Asp Thr Phe Leu Thr Leu Asn Leu Thr Phe Ile Asp Asn Ile Asp
645 650 655

Phe Lys Thr Val Glu Leu Tyr Ser Glu Thr Glu Arg Lys Met Ala Ser
660 665 670

Ala Leu Asp Leu Glu Thr Met Phe Arg Glu Tyr Asn Tyr Tyr Thr Gln
675 680 685

Lys Leu Ala Ser Leu Arg Glu Asp Leu Asp Asn Thr Ile Asp Leu Asn
690 695 700

Arg Asp Arg Leu Val Lys Asp Leu Ser Glu Met Met Ala Asp Leu Gly
705 710 715 720

Asp Ile Gly Lys Val Val Val Asn Thr Phe Ser Gly Ile Val Thr Val
725 730 735

Phe Gly Ser Ile Val Gly Gly Phe Val Ser Phe Phe Thr Asn Pro Ile
740 745 750

Gly Gly Val Thr Ile Ile Leu Leu Leu Ile Val Val Val Phe Val Val
755 760 765

Phe Ile Val Ser Arg Arg Thr Asn Asn Met Asn Glu Ala Pro Ile Lys
770 775 780

Met Ile Tyr Pro Asn Ile Asp Lys Ala Ser Glu Gln Glu Asn Ile Gln
785 790 795 800

Pro Leu Pro Gly Glu Glu Ile Lys Arg Ile Leu Leu Gly Met His Gln
805 810 815

Leu Gln Gln Ser Glu His Gly Lys Ser Glu Glu Glu Ala Ser His Lys
820 825 830

Pro Gly Leu Phe Gln Leu Leu Gly Asp Gly Leu Gln
835 840

<210> 41
<211> 791
<212> PRT
<213> Ateline herpesvirus 3

<400> 41
Met Thr Leu Asn Arg Cys Val Leu Leu Ile Val Leu Thr Phe Ser Thr
1 5 10 15

Ala Cys Ser Gln Thr Thr Pro Ala Ser Ser Asp Glu Asn Gly Lys Thr
20 25 30

Pro Ala Ile Glu Lys Glu Tyr Phe Lys Tyr Arg Val Cys Ser Ala Ser
35 40 45

Thr Thr Gly Glu Leu Phe Arg Phe Asn Leu Asp Arg Ala Cys Pro Ser
50 55 60

Thr Glu Asp Lys Val His Arg Glu Gly Ile Leu Leu Val Tyr Lys Lys
65 70 75 80

Asn Ile Val Pro His Ile Phe Lys Val Arg Arg Tyr Lys Lys Ile Ala
85 90 95

Thr Ser Val Arg Ile Phe Asn Gly Trp Ser Arg Glu Gly Val Ala Ile
100 105 110

Thr Asn Lys Trp Glu Leu Ser Arg Ala Val Pro Lys Tyr Glu Ile Asn
115 120 125

Leu Met Asp Lys Asn Tyr Gln Cys His Asn Cys Met Gln Ile Glu Val
130 135 140

Asn Gly Leu Leu Asn Ser Tyr Cys Asp Arg Asp Gly Asn Asn Lys Thr
145 150 155 160

Val Asp Leu Lys Pro Val Asp Gly Leu Thr Gly Ala Ile Thr Arg Tyr
165 170 175

Val Ser Gln Pro Lys Ile Phe Ala Asp Ala Gly Trp Leu Trp Gly Thr
180 185 190

Tyr Lys Thr Arg Thr Thr Val Asn Cys Glu Ile Val Glu Met Phe Ala
195 200 205

Arg Ser Ala Asp Pro Tyr Thr Tyr Phe Val Thr Ala Leu Gly Asp Thr
210 215 220

Val Glu Val Ser Pro Phe Cys Asp Ala Glu Asn Ser Cys Pro Asn Ala
225 230 235 240

Ser	Asp	Val	Leu	Ser	Ser	Gln	Val	Asp	Phe	Asn	His	Thr	Val	Val	Asp
				245				250						255	
Tyr	Gly	Asn	Arg	Ala	Thr	Ser	Gln	Gln	His	Gly	Lys	Arg	Ile	Phe	Ala
				260				265					270		
His	Thr	Leu	Asp	Tyr	Ser	Val	Ser	Trp	Glu	Ala	Ile	Asn	Lys	Thr	Thr
				275				280				285			
Ser	Val	Cys	Ser	Met	Val	Phe	Trp	Lys	Gly	Phe	Gln	Arg	Ala	Ile	Gln
				290				295			300				
Thr	Glu	His	Asp	Ser	Thr	Tyr	His	Phe	Ile	Ala	Asn	Glu	Ile	Thr	Ala
				305				310			315			320	
Gly	Phe	Ser	Thr	Ser	Lys	Glu	Thr	Leu	Ala	Ser	Phe	Ser	Ser	Glu	Tyr
				325				330			335				
Ser	Cys	Leu	Met	Ser	Asp	Ile	Asn	Ser	Thr	Leu	Thr	Asp	Lys	Ile	Gly
				340				345			350				
Arg	Val	Asn	Asn	Thr	His	Val	Pro	Asn	Gly	Thr	Ala	Gln	Tyr	Phe	Lys
				355				360			365				
Thr	Glu	Gly	Gly	Met	Ile	Leu	Val	Trp	Gln	Pro	Leu	Thr	Ala	Ile	Glu
				370				375			380				
Leu	Glu	Glu	Ala	Met	Ile	Glu	Ala	Thr	Thr	Val	Ser	Pro	Thr	Pro	Leu
				385				390			395			400	
Ser	Thr	Ala	His	Leu	Thr	Ser	Arg	Arg	Thr	Gly	Arg	Arg	Lys	Arg	Asp
				405				410			415				
Val	Ser	Ala	Gly	Ser	Glu	Asn	Ser	Val	Leu	Leu	Ala	Gln	Ile	Gln	Tyr
				420				425			430				
Ala	Tyr	Asp	Lys	Leu	Arg	Gln	Ser	Ile	Asn	Asn	Val	Leu	Glu	Glu	Leu
				435				440			445				
Ala	Ile	Thr	Trp	Cys	Arg	Glu	Gln	Val	Arg	Gln	Thr	Met	Ile	Trp	Tyr
				450				455			460				
Glu	Ile	Ala	Lys	Ile	Asn	Pro	Thr	Ser	Val	Met	Thr	Ala	Ile	Tyr	Gly
				465				470			475			480	
Lys	Pro	Val	Ser	Ala	Lys	Ala	Leu	Gly	Asp	Val	Ile	Ser	Val	Thr	Glu
				485				490			495				
Cys	Ile	Asn	Val	Asp	Gln	Thr	Ser	Val	Ser	Ile	His	Lys	Ser	Leu	Lys
				500				505			510				
Thr	Thr	Asn	Asn	Asp	Val	Cys	Tyr	Ser	Arg	Pro	Pro	Val	Thr	Phe	Lys
				515				520			525				
Phe	Val	Asn	Ser	Ser	Gln	Leu	Phe	Lys	Gly	Gln	Leu	Gly	Ala	Arg	Asn
				530				535			540				

Glu Ile Leu Leu Ser Glu Ser Leu Val Glu Asn Cys His Gln Asn Ala
545 550 555 560

Glu His Phe Phe Thr Ala Lys Asn Glu Thr Tyr His Phe Lys Asn Tyr
565 570 575

Leu His Val Glu Thr Leu Pro Leu Thr Asn Ile Ser Thr Leu Asp Thr
580 585 590

Phe Leu Ala Leu Asn Leu Thr Phe Ile Glu Asn Ile Asp Phe Lys Ala
595 600 605

Val Glu Leu Tyr Ser Ser Gly Glu Arg Lys Leu Ala Asn Val Phe Asp
610 615 620

Leu Glu Thr Met Phe Arg Glu Tyr Asn Tyr Tyr Ala Gln Ser Ile Ser
625 630 635 640

Gly Leu Arg Lys Asp Phe Asp Asn Ser Gln Arg Asn Asn Arg Asp Arg
645 650 655

Ile Ile Gln Asp Phe Ser Glu Ile Leu Ala Asp Leu Gly Ser Ile Gly
660 665 670

Lys Val Ile Val Asn Ile Ala Ser Ser Ala Phe Ser Leu Phe Gly Gly
675 680 685

Ile Val Thr Gly Ile Leu Asn Phe Ile Lys Asn Pro Leu Gly Gly Met
690 695 700

Leu Thr Phe Leu Leu Val Gly Ala Ile Ile Ile Leu Val Ile Leu Leu
705 710 715 720

Val Arg Arg Thr Asn Asn Met Ser Gln Ala Pro Ile Arg Met Ile Tyr
725 730 735

Pro Asp Ile Glu Lys Ser Arg Ser Ser Val Thr Pro Thr Glu Pro Glu
740 745 750

Val Ile Lys Gln Ile Leu Leu Gly Met His Asn Met Gln Gln Glu Glu
755 760 765

Tyr Lys Lys Arg Glu Glu His Lys Ala Ser Gln Pro Ser Phe Leu Lys
770 775 780

Arg Ala Thr Asp Ala Phe Leu
785 790

<210> 42
<211> 792
<212> PRT
<213> Herpesvirus saimiri

<400> 42
Met Val Pro Asn Lys His Leu Leu Leu Ile Ile Leu Ser Phe Ser Thr
1 5 10 15

Ala Cys Gly Gln Thr Thr Pro Thr Thr Ala Val Glu Lys Asn Lys Thr
 20 25 30

Gln Ala Ile Tyr Gln Glu Tyr Phe Lys Tyr Arg Val Cys Ser Ala Ser
 35 40 45

Thr Thr Gly Glu Leu Phe Arg Phe Asp Leu Asp Arg Thr Cys Pro Ser
 50 55 60

Thr Glu Asp Lys Val His Lys Glu Gly Ile Leu Leu Val Tyr Lys Lys
 65 70 75 80

Asn Ile Val Pro Tyr Ile Phe Lys Val Arg Arg Tyr Lys Lys Ile Thr
 85 90 95

Thr Ser Val Arg Ile Phe Asn Gly Trp Thr Arg Glu Gly Val Ala Ile
 100 105 110

Thr Asn Lys Trp Glu Leu Ser Arg Ala Val Pro Lys Tyr Glu Ile Asp
 115 120 125

Ile Met Asp Lys Thr Tyr Gln Cys His Asn Cys Met Gln Ile Glu Val
 130 135 140

Asn Gly Met Leu Asn Ser Tyr Tyr Asp Arg Asp Gly Asn Asn Lys Thr
 145 150 155 160

Val Asp Leu Lys Pro Val Asp Gly Leu Thr Gly Ala Ile Thr Arg Tyr
 165 170 175

Ile Ser Gln Pro Lys Val Phe Ala Asp Pro Gly Trp Leu Trp Gly Thr
 180 185 190

Tyr Arg Thr Arg Thr Thr Val Asn Cys Glu Ile Val Asp Met Phe Ala
 195 200 205

Arg Ser Ala Asp Pro Tyr Thr Tyr Phe Val Thr Ala Leu Gly Asp Thr
 210 215 220

Val Glu Val Ser Pro Phe Cys Asp Val Asp Asn Ser Cys Pro Asn Ala
 225 230 235 240

Thr Asp Val Leu Ser Val Gln Ile Asp Leu Asn His Thr Val Val Asp
 245 250 255

Tyr Gly Asn Arg Ala Thr Ser Gln Gln His Lys Lys Arg Ile Phe Ala
 260 265 270

His Thr Leu Asp Tyr Ser Val Ser Trp Glu Ala Val Asn Lys Ser Ala
 275 280 285

Ser Val Cys Ser Met Val Phe Trp Lys Ser Phe Gln Arg Ala Ile Gln
 290 295 300

Thr Glu His Asp Leu Thr Tyr His Phe Ile Ala Asn Glu Ile Thr Ala
 305 310 315 320

Gly Phe Ser Thr Val Lys Glu Pro Leu Ala Asn Phe Thr Ser Asp Tyr
 325 330 335
 Asn Cys Leu Met Thr His Ile Asn Thr Thr Leu Glu Asp Lys Ile Ala
 340 345 350
 Arg Val Asn Asn Thr His Thr Pro Asn Gly Thr Ala Glu Tyr Tyr Gln
 355 360 365
 Thr Glu Gly Gly Met Ile Leu Val Trp Gln Pro Leu Ile Ala Ile Glu
 370 375 380
 Leu Glu Glu Ala Met Leu Glu Ala Thr Thr Ser Pro Val Thr Pro Ser
 385 390 395 400
 Ala Pro Thr Ser Ser Arg Ser Lys Arg Ala Ile Arg Ser Ile Arg
 405 410 415
 Asp Val Ser Ala Gly Ser Glu Asn Asn Val Phe Leu Ser Gln Ile Gln
 420 425 430
 Tyr Ala Tyr Asp Lys Leu Arg Gln Ser Ile Asn Asn Val Leu Glu Glu
 435 440 445
 Leu Ala Ile Thr Trp Cys Arg Glu Gln Val Arg Gln Thr Met Val Trp
 450 455 460
 Tyr Glu Ile Ala Lys Ile Asn Pro Thr Ser Val Met Thr Ala Ile Tyr
 465 470 475 480
 Gly Lys Pro Val Ser Arg Lys Ala Leu Gly Asp Val Ile Ser Val Thr
 485 490 495
 Glu Cys Ile Asn Val Asp Gln Ser Ser Val Ser Ile His Lys Ser Leu
 500 505 510
 Lys Thr Glu Asn Asn Asp Ile Cys Tyr Ser Arg Pro Pro Val Thr Phe
 515 520 525
 Lys Phe Val Asn Ser Ser Gln Leu Phe Lys Gly Gln Leu Gly Ala Arg
 530 535 540
 Asn Glu Ile Leu Leu Ser Glu Ser Leu Val Glu Asn Cys His Gln Asn
 545 550 555 560
 Ala Glu Thr Phe Phe Thr Ala Lys Asn Glu Thr Tyr His Phe Lys Asn
 565 570 575
 Tyr Val His Val Glu Thr Leu Pro Val Asn Asn Ile Ser Thr Leu Asp
 580 585 590
 Thr Phe Leu Ala Leu Asn Leu Thr Phe Ile Glu Asn Ile Asp Phe Lys
 595 600 605
 Ala Val Glu Leu Tyr Ser Ser Gly Glu Arg Lys Leu Ala Asn Val Phe
 610 615 620

Asp Leu Glu Thr Met Phe Arg Glu Tyr Asn Tyr Tyr Ala Gln Ser Ile
 625 630 635 640

Ser Gly Leu Arg Lys Asp Phe Asp Asn Ser Gln Arg Asn Asn Arg Asp
 645 650 655

Arg Ile Ile Gln Asp Phe Ser Glu Ile Leu Ala Asp Leu Gly Ser Ile
 660 665 670

Gly Lys Val Ile Val Asn Val Ala Ser Gly Ala Phe Ser Leu Phe Gly
 675 680 685

Gly Ile Val Thr Gly Ile Leu Asn Phe Ile Lys Asn Pro Leu Gly Gly
 690 695 700

Met Phe Thr Phe Leu Leu Ile Gly Ala Val Ile Ile Leu Val Ile Leu
 705 710 715 720

Leu Val Arg Arg Thr Asn Asn Met Ser Gln Ala Pro Ile Arg Met Ile
 725 730 735

Tyr Pro Asp Val Glu Lys Ser Lys Ser Thr Val Thr Pro Met Glu Pro
 740 745 750

Glu Thr Ile Lys Gln Ile Leu Leu Gly Met His Asn Met Gln Gln Glu
 755 760 765

Ala Tyr Lys Lys Lys Glu Glu Gln Arg Ala Ala Arg Pro Ser Ile Phe
 770 775 780

Arg Gln Ala Ala Glu Thr Phe Leu
 785 790

<210> 43
 <211> 824
 <212> PRT
 <213> Egyuine herpesvirus 2

<400> 43
 Met Gly Val Gly Gly Pro Arg Val Val Leu Cys Leu Trp Cys Val
 1 5 10 15

Ala Ala Leu Leu Cys Gln Gly Val Ala Gln Glu Val Val Ala Glu Thr
 20 25 30

Thr Thr Pro Phe Ala Thr His Arg Pro Glu Val Val Ala Glu Glu Asn
 35 40 45

Pro Ala Asn Pro Phe Leu Pro Phe Arg Val Cys Gly Ala Ser Pro Thr
 50 55 60

Gly Gly Glu Ile Phe Arg Phe Pro Leu Glu Glu Ser Cys Pro Asn Thr
 65 70 75 80

Glu Asp Lys Asp His Ile Glu Gly Ile Ala Leu Ile Tyr Lys Thr Asn
 85 90 95

Ile Val Pro Tyr Val Phe Asn Val Arg Lys Tyr Arg Lys Ile Met Thr
 100 105 110
 Ser Thr Thr Ile Tyr Lys Gly Trp Ser Glu Asp Ala Ile Thr Asn Gln
 115 120 125
 His Thr Arg Ser Tyr Ala Val Pro Leu Tyr Glu Val Gln Met Met Asp
 130 135 140
 His Tyr Tyr Gln Cys Phe Ser Ala Val Gln Val Asn Glu Gly Gly His
 145 150 155 160
 Val Asn Thr Tyr Tyr Asp Arg Asp Gly Trp Asn Glu Thr Ala Phe Leu
 165 170 175
 Lys Pro Ala Asp Gly Leu Thr Ser Ser Ile Thr Arg Tyr Gln Ser Gln
 180 185 190
 Pro Glu Val Tyr Ala Thr Pro Arg Asn Leu Leu Trp Ser Tyr Thr Thr
 195 200 205
 Arg Thr Thr Val Asn Cys Glu Val Thr Glu Met Ser Ala Arg Ser Met
 210 215 220
 Lys Pro Phe Glu Phe Phe Val Thr Ser Val Gly Asp Thr Ile Glu Met
 225 230 235 240
 Ser Pro Phe Leu Lys Glu Asn Gly Thr Glu Pro Glu Lys Ile Leu Lys
 245 250 255
 Arg Pro His Ser Ile Gln Leu Leu Lys Asn Tyr Ala Val Thr Lys Tyr
 260 265 270
 Gly Val Gly Leu Gly Gln Ala Asp Asn Ala Thr Arg Phe Phe Ala Ile
 275 280 285
 Phe Gly Asp Tyr Ser Leu Ser Trp Lys Ala Thr Thr Glu Asn Ser Ser
 290 295 300
 Tyr Cys Asp Leu Ile Leu Trp Lys Gly Phe Ser Asn Ala Ile Gln Thr
 305 310 315 320
 Gln His Asn Ser Ser Leu His Phe Ile Ala Asn Asp Ile Thr Ala Ser
 325 330 335
 Phe Ser Thr Pro Leu Glu Glu Ala Asn Phe Asn Glu Thr Phe Lys
 340 345 350
 Cys Ile Trp Asn Asn Thr Gln Glu Glu Ile Gln Lys Lys Leu Lys Glu
 355 360 365
 Val Glu Lys Thr His Arg Pro Asn Gly Thr Ala Lys Val Tyr Lys Thr
 370 375 380
 Thr Gly Asn Leu Tyr Ile Val Trp Gln Pro Leu Ile Gln Ile Asp Leu
 385 390 395 400

Leu Asp Thr His Ala Lys Leu Tyr Asn Leu Thr Asn Ala Thr Ala Ser
 405 410 415
 Pro Thr Ser Thr Pro Thr Ser Pro Arg Arg Arg Arg Arg Asp Thr
 420 425 430
 Ser Ser Val Ser Gly Gly Asn Asn Gly Asp Asn Ser Thr Lys Glu
 435 440 445
 Glu Ser Val Ala Ala Ser Gln Val Gln Phe Ala Tyr Asp Asn Leu Arg
 450 455 460
 Lys Ser Ile Asn Arg Val Leu Gly Glu Leu Ser Arg Ala Trp Cys Arg
 465 470 475 480
 Glu Gln Tyr Arg Ala Ser Leu Met Trp Tyr Glu Leu Ser Lys Ile Asn
 485 490 495
 Pro Thr Ser Val Met Ser Ala Ile Tyr Gly Arg Pro Val Ser Ala Lys
 500 505 510
 Leu Ile Gly Asp Val Val Ser Val Ser Asp Cys Ile Ser Val Asp Gln
 515 520 525
 Lys Ser Val Phe Val His Lys Asn Met Lys Val Pro Gly Lys Glu Asp
 530 535 540
 Leu Cys Tyr Thr Arg Pro Val Val Gly Phe Lys Phe Ile Asn Gly Ser
 545 550 555 560
 Glu Leu Phe Ala Gly Gln Leu Gly Pro Arg Asn Glu Ile Val Leu Ser
 565 570 575
 Thr Ser Gln Val Glu Val Cys Gln His Ser Cys Glu His Tyr Phe Gln
 580 585 590
 Ala Gly Asn Gln Met Tyr Lys Tyr Lys Asp Tyr Tyr Tyr Val Ser Thr
 595 600 605
 Leu Asn Leu Thr Asp Ile Pro Thr Leu His Thr Met Ile Thr Leu Asn
 610 615 620
 Leu Ser Leu Val Glu Asn Ile Asp Phe Lys Val Ile Glu Leu Tyr Ser
 625 630 635 640
 Lys Thr Glu Lys Arg Leu Ser Asn Val Phe Asp Ile Glu Thr Met Phe
 645 650 655
 Arg Glu Tyr Asn Tyr Tyr Thr Gln Asn Leu Asn Gly Leu Arg Lys Asp
 660 665 670
 Leu Asp Asp Ser Ile Asp His Gly Arg Asp Ser Phe Ile Gln Thr Leu
 675 680 685
 Gly Asp Ile Met Gln Asp Leu Gly Thr Ile Gly Lys Val Val Val Asn
 690 695 700

Val	Ala	Ser	Gly	Val	Phe	Ser	Leu	Phe	Gly	Ser	Ile	Val	Ser	Gly	Val
705				710					715				720		
Ile	Ser	Phe	Phe	Lys	Asn	Pro	Phe	Gly	Gly	Met	Leu	Leu	Ile	Val	Leu
		725					730						735		
Ile	Ile	Ala	Gly	Val	Val	Val	Tyr	Leu	Phe	Met	Thr	Arg	Ser	Arg	
		740			745							750			
Ser	Ile	Tyr	Ser	Ala	Pro	Ile	Arg	Met	Leu	Tyr	Pro	Gly	Val	Glu	Arg
		755			760			765							
Ala	Ala	Gln	Glu	Pro	Gly	Ala	His	Pro	Val	Ser	Glu	Asp	Gln	Ile	Arg
		770			775			780							
Asn	Ile	Leu	Met	Gly	Met	His	Gln	Phe	Gln	Gln	Arg	Gln	Arg	Ala	Glu
		785			790			795					800		
Glu	Glu	Ala	Arg	Arg	Glu	Glu	Glu	Val	Lys	Gly	Lys	Arg	Thr	Leu	Phe
		805				810						815			
Glu	Val	Ile	Arg	Asp	Ser	Ala	Thr								
		820													
<210>	44														
<211>	818														
<212>	PRT														
<213>	Equine herpesvirus	5													
<400>	44														
Met	Val	Ala	Trp	Phe	Gly	Leu	Trp	Gly	Phe	Ala	Arg	Leu	Met	Ala	Thr
1				5				10					15		
Leu	Ala	Leu	Leu	Cys	Gly	Arg	Val	Ala	Leu	Asp	Glu	Ser	Ser	Ala	Thr
				20				25					30		
Pro	Ser	Ile	Pro	Pro	Thr	His	Lys	Pro	Ala	Val	His	His	Glu	Asp	Asn
		35			40						45				
Thr	Thr	Asn	Pro	Phe	Leu	Leu	Phe	Arg	Val	Cys	Gly	Ala	Ser	Pro	Thr
		50			55			60							
Gly	Glu	Ile	Phe	Arg	Phe	Pro	Leu	Glu	Glu	Asn	Cys	Pro	Asn	Thr	Glu
		65			70			75					80		
Asp	Lys	Glu	His	Val	Glu	Gly	Ile	Leu	Leu	Ile	Tyr	Lys	Thr	Asn	Ile
		85				90						95			
Val	Pro	Tyr	Ile	Phe	Asn	Val	Arg	Lys	Tyr	Arg	Lys	Leu	Val	Thr	Ser
			100			105						110			
Thr	Thr	Ile	Tyr	Lys	Gly	Trp	Ser	Gln	Asp	Ala	Ile	Thr	Asn	Gln	Tyr
		115				120						125			
Thr	Ser	Ser	Phe	Ala	Met	Pro	Leu	Trp	Glu	Ala	Arg	Leu	Val	Asp	Tyr
		130				135			140						

Asn	Tyr	Glu	Cys	Tyr	Asn	Gly	Ile	Gln	Val	Thr	Glu	Asn	Gly	His	Leu
145					150					155				160	
Thr	Thr	Tyr	Val	Asp	Arg	Asp	Gly	Tyr	Asn	Glu	Ser	Val	Arg	Leu	Val
				165					170				175		
Pro	Ala	Asp	Gly	Leu	Thr	Ser	Ser	Ile	Arg	Arg	Tyr	His	Ser	Gln	Pro
				180				185				190			
Glu	Leu	Tyr	Val	Thr	Pro	Arg	Asn	Leu	Leu	Trp	Ser	Tyr	Thr	Thr	Arg
				195				200				205			
Thr	Thr	Val	Asn	Cys	Glu	Val	Ile	Asp	Met	Thr	Ala	Arg	Ser	His	Lys
					210		215			220					
Pro	Phe	Glu	Tyr	Phe	Val	Thr	Ala	Ser	Gly	Asp	Ser	Ile	Glu	Thr	Ser
				225			230			235			240		
Pro	Phe	Tyr	Thr	Asn	Ala	Ser	Arg	Arg	Val	Pro	Val	Gln	Val	Leu	Tyr
				245					250				255		
Asn	Tyr	Ser	Val	Thr	Asp	Tyr	Gly	Val	Gly	Leu	Gly	Ser	Gly	Glu	Asn
				260				265				270			
Val	Thr	Arg	Phe	Phe	Ala	Thr	Leu	Asn	Asp	Phe	Ser	Ile	Ser	Trp	Lys
				275			280				285				
Ala	Ala	Thr	Glu	Asn	Ser	Ser	Tyr	Cys	Pro	Leu	Val	Leu	Trp	Lys	Gly
				290			295				300				
Phe	Pro	Ser	Ala	Ile	Gln	Thr	Lys	His	Glu	Lys	Ser	Tyr	His	Phe	Ile
				305			310			315			320		
Ala	Asp	Ala	Val	Thr	Ala	Ser	Phe	Thr	Thr	Pro	Leu	Thr	Asp	Glu	Thr
				325				330				335			
Ser	Tyr	Phe	Asn	Thr	Thr	Tyr	Gln	Cys	Ala	Trp	Gln	Asp	Ile	Glu	Gly
				340				345				350			
Glu	Ile	Gln	Lys	Arg	Phe	Asp	Pro	Val	Ser	Lys	Thr	His	Ala	Arg	Asn
				355				360			365				
Gly	Ser	Val	Gln	Ile	Tyr	Lys	Thr	Ser	Gly	Asn	Leu	Tyr	Val	Val	Trp
				370			375			380					
Gln	Pro	Leu	Val	Gln	Leu	Asp	Leu	Leu	Ala	Ala	His	Ala	Lys	Thr	Ile
				385			390			395			400		
Asn	Ser	Thr	Asp	Asn	Ser	Thr	Ser	Pro	Thr	Thr	Ala	Pro	Asn	Thr	Thr
				405				410				415			
Thr	Ser	Thr	Ser	Ser	Arg	Arg	Lys	Arg	Arg	Asp	Thr	Gly	Asn	Thr	Ala
				420				425				430			
Thr	Asn	Asn	Ser	Ser	Asn	Asn	Ser	Ser	Met	Glu	Glu	Asn	Leu	Ala	
				435				440			445				

Thr Ser Gln Val Gln Phe Ala Tyr Asp Gln Leu Arg Lys Ser Ile Asn
 450 455 460
 Arg Val Leu Glu Gln Leu Ser Arg Val Trp Cys Gln Asn Gln Tyr Arg
 465 470 475 480
 Ala Ser Leu Met Trp Tyr Glu Leu Ser Lys Ile Asn Pro Thr Ser Val
 485 490 495
 Met Ser Ala Ile Tyr Gly Arg Pro Val Ser Ala Lys Leu Val Gly Asp
 500 505 510
 Val Val Gln Ile Ser Asp Cys Ile Thr Val Asp Gln Glu Ser Val Phe
 515 520 525
 Val His Arg Asn Leu Arg Val Pro Gly Ser Lys Asp Leu Cys Tyr Thr
 530 535 540
 Arg Pro Val Val Gly Phe Lys Phe Ile Asn Gly Ser Glu Leu Phe Val
 545 550 555 560
 Gly Gln Leu Gly Ala Arg Asn Glu Ile Leu Leu Ser Thr Asn Leu Val
 565 570 575
 Glu Val Cys Gln His Ser Cys Glu His Tyr Phe Gln Gly Gly Asn His
 580 585 590
 Ile Tyr Lys Tyr Lys Asn Tyr Glu Tyr Val Ser Thr Met Asn Leu Thr
 595 600 605
 Asp Val Pro Thr Leu His Thr Met Ile Thr Leu Asn Leu Ser Leu Val
 610 615 620
 Glu Asn Val Asp Phe Gln Val Ile Gln Leu Tyr Ser Gln Lys Glu Lys
 625 630 635 640
 Lys Leu Ser Asn Val Phe Asp Ile Glu Thr Met Phe Arg Glu Tyr Asn
 645 650 655
 Tyr Tyr Thr Gln Asn Leu Lys Gly Leu Arg Lys Asp Leu Asp Asp Ser
 660 665 670
 Ile His Asp Gly Arg Asp Ser Phe Ile Gln Phe Leu Gly Asp Leu Val
 675 680 685
 Gln Asp Leu Val Pro Val Gly Asp Val Ile Val Asn Val Ala Ser Gly
 690 695 700
 Val Phe Ser Leu Phe Gly Ser Ile Val Ser Gly Val Ile Ser Phe Leu
 705 710 715 720
 Lys Asn Pro Leu Gly Ala Ile Leu Thr Ile Ala Leu Ile Val Gly Gly
 725 730 735
 Ile Ile Val Leu Tyr Leu Phe Ile Thr Arg Ser Arg Thr Val Tyr Gln
 740 745 750

Ala Pro Ile Arg Met Leu Tyr Pro Glu Val Asp Arg Ala Pro Gln Gln
755 760 765

Asn Val Gln Pro Ile Pro Glu Asp Gln Val Arg Ser Ile Leu Leu Ala
770 775 780

Met His Gln Phe Gln
785 790 795 800

Glu Glu His Thr Gln Arg Arg Ser Ile Phe Asp Thr Ile Arg Glu Ser
805 810 815

Thr Ser

<210> 45

<211> 830

<212> PRT

<213> Alcelaphine herpesvirus

<400> 45

Met Ala His Thr Gly Ser Thr Val Cys Ala Phe Leu Ile Phe Ala Val
1 5 10 . 15

Leu Lys Asn Val Phe Cys Gln Thr Pro Thr Ser Ser Ser Glu Val Glu
20 25 30

Asp Val Ile Pro Glu Ala Asn Thr Val Ser Asp Asn Ile Ile Arg Gln
35 40 45

Gln Arg Asn Asn Thr Ala Lys Gly Ile His Ser Asp Pro Ser Ala Phe
50 55 60

Pro Phe Arg Val Cys Ser Ala Ser Asn Ile Gly Asp Ile Phe Arg Phe
65 70 75 80

Gln Thr Ser His Ser Cys Pro Asn Thr Lys Asp Lys Glu His Asn Glu
85 90 95

Gly Ile Leu Leu Ile Phe Lys Glu Asn Ile Val Pro Tyr Val Phe Lys
100 105 110

Val Arg Lys Tyr Arg Lys Ile Val Thr Thr Ser Thr Ile Tyr Asn Gly
115 120 125

Ile Tyr Ala Asp Ala Val Thr Asn Gln His Val Phe Ser Lys Ser Val
130 135 140

Pro Ile Tyr Glu Thr Arg Arg Met Asp Thr Ile Tyr Gln Cys Tyr Asn
145 150 155 160

Ser Leu Asp Val Thr Val Gly Gly Asn Leu Leu Val Tyr Thr Asp Asn
165 170 175

Asp Gly Ser Asn Met Thr Val Asp Leu Gln Pro Val Asp Gly Leu Ser
180 185 190

Asn Ser Val Arg Arg Tyr His Ser Gln Pro Glu Ile His Ala Glu Pro
 195 200 205
 Gly Trp Leu Leu Gly Gly Tyr Arg Arg Arg Thr Thr Val Asn Cys Glu
 210 215 220
 Val Thr Glu Thr Asp Ala Arg Ala Val Pro Pro Phe Arg Tyr Phe Ile
 225 230 235 240
 Thr Asn Ile Gly Asp Thr Ile Glu Met Ser Pro Phe Trp Ser Lys Ala
 245 250 255
 Trp Asn Glu Thr Glu Phe Ser Gly Glu Pro Asp Arg Thr Leu Thr Val
 260 265 270
 Ala Lys Asp Tyr Arg Val Val Asp Tyr Lys Phe Arg Gly Thr Gln Pro
 275 280 285
 Gln Gly His Thr Arg Ile Phe Val Asp Lys Glu Glu Tyr Thr Leu Ser
 290 295 300
 Trp Ala Gln Gln Phe Arg Asn Ile Ser Tyr Cys Arg Trp Ala His Trp
 305 310 315 320
 Lys Ser Phe Asp Asn Ala Ile Lys Thr Glu His Gly Lys Ser Leu His
 325 330 335
 Phe Val Ala Asn Asp Ile Thr Ala Ser Phe Tyr Thr Pro Asn Thr Gln
 340 345 350
 Thr Arg Glu Val Leu Gly Lys His Val Cys Leu Asn Asn Thr Ile Glu
 355 360 365
 Ser Glu Leu Lys Ser Arg Leu Ala Lys Val Asn Asp Thr His Ser Pro
 370 375 380
 Asn Gly Thr Ala Gln Tyr Tyr Leu Thr Asn Gly Gly Leu Leu Leu Val
 385 390 395 400
 Trp Gln Pro Leu Val Gln Gln Lys Leu Leu Asp Ala Lys Gly Leu Leu
 405 410 415
 Asp Ala Val Lys Lys Gln Gln Asn Thr Thr Thr Thr Thr Thr Thr
 420 425 430
 Arg Ser Arg Arg Gln Arg Arg Ser Val Ser Ser Gly Ile Asp Asp Val
 435 440 445
 Tyr Thr Ala Glu Ser Thr Ile Leu Leu Thr Gln Ile Gln Phe Ala Tyr
 450 455 460
 Asp Thr Leu Arg Ala Gln Ile Asn Asn Val Leu Glu Glu Leu Ser Arg
 465 470 475 480
 Ala Trp Cys Arg Glu Gln His Arg Ala Ser Leu Met Trp Asn Glu Leu
 485 490 495

Ser Lys Ile Asn Pro Thr Ser Val Met Ser Ser Ile Tyr Gly Arg Pro
500 505 510

Val Ser Ala Lys Arg Ile Gly Asp Val Ile Ser Val Ser His Cys Val
515 520 525

Val Val Asp Gln Asp Ser Val Ser Leu His Arg Ser Met Arg Val Pro
530 535 540

Gly Arg Asp Lys Thr His Glu Cys Tyr Ser Arg Pro Pro Val Thr Phe
545 550 555 560

Lys Phe Ile Asn Asp Ser His Leu Tyr Lys Gly Gln Leu Gly Val Asn
565 570 575

Asn Glu Ile Leu Leu Thr Thr Ala Val Glu Ile Cys His Glu Asn
580 585 590

Thr Glu His Tyr Phe Gln Gly Gly Asn Asn Met Tyr Phe Tyr Lys Asn
595 600 605

Tyr Arg His Val Lys Thr Met Pro Val Gly Asp Val Ala Thr Leu Asp
610 615 620

Thr Phe Met Val Leu Asn Leu Thr Leu Val Glu Asn Ile Asp Phe Gln
625 630 635 640

Val Ile Glu Leu Tyr Ser Arg Glu Glu Lys Arg Met Ser Thr Ala Phe
645 650 655

Asp Ile Glu Thr Met Phe Arg Glu Tyr Asn Tyr Tyr Thr Gln Arg Val
660 665 670

Thr Gly Leu Arg Arg Asp Leu Thr Asp Leu Ala Thr Asn Arg Asn Gln
675 680 685

Phe Val Asp Ala Phe Gly Ser Leu Met Asp Asp Leu Gly Val Val Gly
690 695 700

Lys Thr Val Leu Asn Ala Val Ser Ser Val Ala Thr Leu Phe Ser Ser
705 710 715 720

Ile Val Ser Gly Ile Ile Asn Phe Ile Lys Asn Pro Phe Gly Gly Met
725 730 735

Leu Leu Phe Gly Leu Ile Ala Ala Val Val Ile Thr Val Ile Leu Leu
740 745 750

Asn Arg Lys Ala Lys Arg Phe Ala Gln Asn Pro Val Gln Met Ile Tyr
755 760 765

Pro Asp Ile Lys Thr Ile Thr Ser Gln Arg Glu Glu Leu Gln Val Asp
770 775 780

Pro Ile Ser Lys His Glu Leu Asp Arg Ile Met Leu Ala Met His Asp
785 790 795 800

Tyr His Ala Ser Lys Gln Pro Glu Ser Lys Gln Asp Glu Glu Gln Gly
 805 810 815
 Ser Thr Thr Ser Gly Pro Ala Asp Trp Leu Asn Lys Ala Lys
 820 825 830
 <210> 46
 <211> 829
 <212> PRT
 <213> Epstein-Barr virus
 <400> 46
 Met Thr Arg Arg Arg Val Leu Ser Val Val Val Leu Leu Ala Ala Leu
 1 5 10 15
 Ala Cys Arg Leu Gly Ala Gln Thr Pro Glu Gln Pro Ala Pro Pro Ala
 20 25 30
 Thr Thr Val Gln Pro Thr Ala Thr Arg Gln Gln Thr Ser Phe Pro Phe
 35 40 45
 Arg Val Cys Glu Leu Ser Ser His Gly Asp Leu Phe Arg Phe Ser Ser
 50 55 60
 Asp Ile Gln Cys Pro Ser Phe Gly Thr Arg Glu Asn His Thr Glu Gly
 65 70 75 80
 Leu Leu Met Val Phe Lys Asp Asn Ile Ile Pro Tyr Ser Phe Lys Val
 85 90 95
 Arg Ser Tyr Thr Lys Ile Val Thr Asn Ile Leu Ile Tyr Asn Gly Trp
 100 105 110
 Tyr Ala Asp Ser Val Thr Asn Arg His Glu Glu Lys Phe Ser Val Asp
 115 120 125
 Ser Tyr Glu Thr Asp Gln Met Asp Thr Ile Tyr Gln Cys Tyr Asn Ala
 130 135 140
 Val Lys Met Thr Lys Asp Gly Leu Thr Arg Val Tyr Val Asp Arg Asp
 145 150 155 160
 Gly Val Asn Ile Thr Val Asn Leu Lys Pro Thr Gly Gly Leu Ala Asn
 165 170 175
 Gly Val Arg Arg Tyr Ala Ser Gln Thr Glu Leu Tyr Asp Ala Pro Gly
 180 185 190
 Trp Leu Ile Trp Thr Tyr Arg Thr Arg Thr Val Asn Cys Leu Ile
 195 200 205
 Thr Asp Met Met Ala Lys Ser Asn Ser Pro Phe Asp Phe Phe Val Thr
 210 215 220
 Thr Thr Gly Gln Thr Val Glu Met Ser Pro Phe Tyr Asp Gly Lys Asn
 225 230 235 240

Lys Glu Thr Phe His Glu Arg Ala Asp Ser Phe His Val Arg Thr Asn
245 250 255

Tyr Lys Ile Val Asp Tyr Asp Asn Arg Gly Thr Asn Pro Gln Gly Glu
260 265 270

Arg Arg Ala Phe Leu Asp Lys Gly Thr Tyr Thr Leu Ser Trp Lys Leu
275 280 285

Glu Asn Arg Thr Ala Tyr Cys Pro Leu Gln His Trp Gln Thr Phe Asp
290 295 300

Ser Thr Ile Ala Thr Glu Thr Gly Lys Ser Ile His Phe Val Thr Asp
305 310 315 320

Glu Gly Thr Ser Ser Phe Val Thr Asn Thr Thr Val Gly Ile Glu Leu
325 330 335

Pro Asp Ala Phe Lys Cys Ile Glu Glu Gln Val Asn Lys Thr Met His
340 345 350

Glu Lys Tyr Glu Ala Val Gln Asp Arg Tyr Thr Lys Gly Gln Glu Ala
355 360 365

Ile Thr Tyr Phe Ile Thr Ser Gly Gly Leu Leu Leu Ala Trp Leu Pro
370 375 380

Leu Thr Pro Arg Ser Leu Ala Thr Val Lys Asn Leu Thr Glu Leu Thr
385 390 395 400

Thr Pro Thr Ser Ser Pro Pro Ser Ser Pro Ser Pro Pro Ala Pro Ser
405 410 415

Ala Ala Arg Gly Ser Thr Pro Ala Ala Val Leu Arg Arg Arg Arg Arg
420 425 430

Asp Ala Gly Asn Ala Thr Thr Pro Val Pro Pro Thr Ala Pro Gly Lys
435 440 445

Ser Leu Gly Thr Leu Asn Asn Pro Ala Thr Val Gln Ile Gln Phe Ala
450 455 460

Tyr Asp Ser Leu Arg Arg Gln Ile Asn Arg Met Leu Gly Asp Leu Ala
465 470 475 480

Arg Ala Trp Cys Leu Glu Gln Lys Arg Gln Asn Met Val Leu Arg Glu
485 490 495

Leu Thr Lys Ile Asn Pro Thr Thr Val Met Ser Ser Ile Tyr Gly Lys
500 505 510

Ala Val Ala Ala Lys Arg Leu Gly Asp Val Ile Ser Val Ser Gln Cys
515 520 525

Val Pro Val Asn Gln Ala Thr Val Thr Leu Arg Lys Ser Met Arg Val
530 535 540

Pro Gly Ser Glu Thr Met Cys Tyr Ser Arg Pro Leu Val Ser Phe Ser
545 550 555 560

Phe Ile Asn Asp Thr Lys Thr Tyr Glu Gly Gln Leu Gly Thr Asp Asn
565 570 575

Glu Ile Phe Leu Thr Lys Lys Met Thr Glu Val Cys Gln Ala Thr Ser
580 585 590

Gln Tyr Tyr Phe Gln Ser Gly Asn Glu Ile His Val Tyr Asn Asp Tyr
595 600 605

His His Phe Lys Thr Ile Glu Leu Asp Gly Ile Ala Thr Leu Gln Thr
610 615 620

Phe Ile Ser Leu Asn Thr Ser Leu Ile Glu Asn Ile Asp Phe Ala Ser
625 630 635 640

Leu Glu Leu Tyr Ser Arg Asp Glu Gln Arg Ala Ser Asn Val Phe Asp
645 650 655

Leu Glu Gly Ile Phe Arg Glu Tyr Asn Phe Gln Ala Gln Asn Ile Ala
660 665 670

Gly Leu Arg Lys Asp Leu Asp Asn Ala Val Ser Asn Gly Arg Asn Gln
675 680 685

Phe Val Asp Gly Leu Gly Glu Leu Met Asp Ser Leu Gly Ser Val Gly
690 695 700

Gln Ser Ile Thr Asn Leu Val Ser Thr Val Gly Gly Leu Phe Ser Ser
705 710 715 720

Leu Val Ser Gly Phe Ile Ser Phe Phe Lys Asn Pro Phe Gly Gly Met
725 730 735

Leu Ile Leu Val Leu Val Ala Gly Val Val Ile Leu Val Ile Ser Leu
740 745 750

Thr Arg Arg Thr Arg Gln Met Ser Gln Gln Pro Val Gln Met Leu Tyr
755 760 765

Pro Gly Ile Asp Glu Leu Ala Gln Gln His Ala Ser Gly Glu Gly Pro
770 775 780

Gly Ile Asn Pro Ile Ser Lys Thr Glu Leu Gln Ala Ile Met Leu Ala
785 790 795 800

Leu His Glu Gln Asn Gln Glu Gln Lys Arg Ala Ala Gln Arg Ala Ala
805 810 815

Gly Pro Ser Val Ala Ser Arg Ala Leu Gln Ala Ala Arg
820 825

<210> 47
<211> 660
<212> DNA

<213> artificial

<220>

<223> Suid herpesvirus 1 - bases 641-1300

<400> 47

cgccgcccgtc	cggtccacg	gtggtcggc	tggagcccga	gcaggcctgc	cccgagtact	60
cgcaggggac	caacttcacg	gaggggatcg	ccgtgcttt	caaggagaac	atcgccccgc	120
acaagttcaa	ggcccacatc	tactacaaga	acgtcatcg	cacgaccgtg	tggtccggaa	180
gcacgtacgc	ggccatcacg	aaccgttca	cagaccgt	gcccgtcccc	gtgcaggaga	240
tcacggacgt	gatcgaccgc	cgcggcaagt	gcgtctcaa	ggccgagtagc	gtgcgcaaca	300
accacaagg	gaccgccttc	gaccgcgacg	agaacccgt	cgaggtggac	ctgcgcccct	360
cgccctgaa	cgcgctcggc	acccgcggct	ggcacaccac	caacgcacacc	tacaccaaga	420
tcggcgccgc	gggcttctac	cacacggca	cctccgtcaa	ctgcatcg	gaggaggtgg	480
aggcgcgctc	cgtgtacccc	tacgactct	tcgcctgtc	cacggggac	attgttaca	540
tgtccccctt	ctacggcctg	cgcgaggggg	cccacggga	gcacatcg	tacgcgccc	600
ggcgcttcca	gcaggtggag	cactactacc	ccatcgac	ggactcg	ctccgcgc	660

<210> 48

<211> 359

<212> PRT

<213> artificial

<220>

<223> Suid herpesvirus 1 - bases 491-850

<400> 48

Ala	Ala	Pro	Ala	Ala	Ala	Arg	Arg	Ala	Arg	Arg	Ser	Pro	Gly	Pro	Ala
1						5			10					15	

Gly	Thr	Pro	Glu	Pro	Pro	Ala	Val	Asn	Gly	Thr	Gly	His	Leu	Arg	Ile
										20			25		30

Thr	Thr	Gly	Ser	Ala	Glu	Phe	Ala	Arg	Leu	Gln	Phe	Thr	Tyr	Asp	His
										35			40		45

Ile	Gln	Ala	His	Val	Asn	Asp	Met	Leu	Gly	Arg	Ile	Ala	Ala	Trp
							50		55				60	

Cys	Glu	Leu	Gln	Asn	Lys	Asp	Arg	Thr	Leu	Trp	Ser	Glu	Met	Ser	Arg
							65		70			75		80	

Leu	Asn	Pro	Ser	Ala	Val	Ala	Thr	Ala	Ala	Leu	Gly	Gln	Arg	Val	Ser
							85			90			95		

Ala	Arg	Met	Leu	Gly	Asp	Val	Met	Ala	Ile	Ser	Arg	Cys	Val	Glu	Val
							100		105				110		

Arg	Gly	Gly	Val	Tyr	Val	Gln	Asn	Ser	Met	Arg	Val	Pro	Gly	Glu	Arg
							115		120			125			

Gly	Thr	Cys	Tyr	Ser	Arg	Pro	Leu	Val	Thr	Phe	Glu	His	Asn	Gly	Thr
							130		135			140			

Gly	Val	Ile	Glu	Gly	Gln	Leu	Gly	Asp	Asp	Asn	Glu	Leu	Leu	Ile	Ser
							145		150			155		160	

Arg Asp Leu Ile Glu Pro Cys Thr Gly Asn His Arg Arg Tyr Phe Lys
165 170 175

Leu Gly Ser Gly Tyr Val Tyr Tyr Glu Asp Tyr Asn Tyr Val Arg Met
180 185 190

Val Glu Val Pro Glu Thr Ile Ser Thr Arg Val Thr Leu Asn Leu Thr
195 200 205

Leu Leu Glu Asp Arg Glu Phe Leu Pro Leu Glu Val Tyr Thr Arg Glu
210 215 220

Glu Leu Ala Asp Thr Gly Leu Leu Asp Tyr Ser Glu Ile Gln Arg Arg
225 230 235 240

Asn Gln Leu His Ala Leu Lys Phe Tyr Asp Ile Asp Arg Val Val Lys
245 250 255

Val Asp His Asn Val Val Leu Leu Arg Gly Ile Ala Asn Phe Phe Gln
260 265 270

Gly Leu Gly Asp Val Gly Ala Ala Val Gly Lys Val Val Leu Gly Ala
275 280 285

Thr Gly Ala Val Ile Ser Ala Val Gly Gly Met Val Ser Phe Leu Ser
290 295 300

Asn Pro Phe Gly Ala Leu Ala Ile Gly Leu Leu Val Leu Ala Gly Leu
305 310 315 320

Val Ala Ala Phe Leu Ala Tyr Arg His Ile Ser Arg Leu Arg Arg Asn
325 330 335

Pro Met Lys Ala Leu Tyr Pro Val Thr Thr Lys Thr Leu Lys Glu Asp
340 345 350

Gly Val Asp Glu Gly Asp Val
355

<210> 49

<211> 420

<212> DNA

<213> Suid herpesvirus 2

<400> 49

ccagcataat	gatagccaat	aatctgtgtt	actctaccct	gatcttaaat	gacgaggacg	60
tgacggggat	cgacgagaaa	gatattctga	cggtgcattgt	aaacaagaat	accgtgtaca	120
ggttcgtag	gaggcgcgtc	agggagtcata	tactcggcac	gctgctgtct	agatggctca	180
ggaagagaaa	ggaagtgaag	gcgcgcatga	aacgctgtga	ggaccctatg	ttggcactga	240
tacttgacaa	gcagcagctt	gccctcaagg	tgacgtgcaa	tgcgtttac	ggcttcacgg	300
gagccgtgca	cggctgtctg	ccgtgtctcc	ctctagcggc	gtccatcacc	agcatagggc	360
gggacatgct	taggcagacg	agtgacttta	tcaacaatgt	ccttcgtct	agagaatacg	420

<210> 50

<211> 159

<212> PRT

<213> Suid herpesvirus 2

<400> 50

Ser Ile Met Ile Ala Asn Asn Leu Cys Tyr Ser Thr Leu Ile Leu Asn
1 5 10 15

Asp Glu Asp Val Thr Gly Ile Asp Glu Lys Asp Ile Leu Thr Val His
20 25 30

Val Asn Lys Asn Thr Val Tyr Arg Phe Val Arg Ser Ser Val Arg Glu
35 40 45

Ser Ile Leu Gly Thr Leu Leu Ser Arg Trp Leu Arg Lys Arg Lys Glu
50 55 60

Val Lys Ala Arg Met Lys Arg Cys Glu Asp Pro Met Leu Ala Leu Ile
65 70 75 80

Leu Asp Lys Gln Gln Leu Ala Leu Lys Val Thr Cys Asn Ala Phe Tyr
85 90 95

Gly Phe Thr Gly Ala Val His Gly Leu Leu Pro Cys Leu Pro Leu Ala
100 105 110

Ala Ser Ile Thr Ser Ile Gly Arg Asp Met Leu Arg Gln Thr Ser Asp
115 120 125

Phe Ile Asn Asn Val Leu Ser Ser Arg Glu Tyr Val Ser Glu Lys Phe
130 135 140

Ser Leu Ser Asp Gly Asp Phe Gln Gly Asp Phe Ser Pro Glu Cys
145 150 155

<210> 51

<211> 466

<212> DNA

<213> artificial

<220>

<223> Portion of porcine gamma herpesvirus polymerase - AF118399

<400> 51

taatctatgt cactctaccc taatccatca tgaagacctg cataaaatatac ctcaattaaa 60
ggaggaggat tatgaaacat ttttgattag ttctggcct gttcactttg taaaaaaaaaca 120
catatcagaa tctcttctgt ctaacctgct tacaacatgg ctggctaaaga gaaaaatgat 180
cagaaaaggaa ttagcagcat gtgctgaccc aaagctcagg acaatttttag ataaacagca 240
gcttgcaatt aaggtgacat gcaatgctgt gtatgggttc actgggttg catctggtat 300
gctgcccctgt ctcaagattg cagagaccat aactatgcaa ggaaggggcca tggggaaaa 360
gacaaaagta tttgttagaga atttaagtca tgaggatctc cattccatct gtaaggttgg 420
ctttatgcct cagtccacca acagcattga taaacccttc aaggtg 466

<210> 52

<211> 423

<212> DNA

<213> artificial

<220>

<223> Portion of porcine gamma herpesvirus polymerase - AF118401

<400> 52

gaggacctgc	ataagtatcc	tcaattaaag	gaggatgatt	atgaaacatt	tttgattagt	60
tctggccctg	ttcactttg	aaaaaaacac	atatcagaat	ctcttctgtc	gaacttgctc	120
acaacatggc	tggccaagag	aaaaatgatc	agaaaggaat	tgacagcatg	tgctgatcca	180
aagctcagga	caattttaga	aaaacagcag	cttgcattt	aggtgacatg	caatgctgt	240
tatggattca	ctgggttgc	atctggatg	ctgcatgtc	tcaagattgc	agagaccatc	300
actatgcaag	gaagggccat	gttggaaaag	acaaaagtat	tttgtagagaa	tctgagtcat	360
gaagatctcc	gttccatatg	taaggttggc	tctatacctc	agtcatcaaa	cgtgtttgat	420
aaa						423

<210> 53

<211> 292

<212> DNA

<213> artificial

<220>

<223> Portion of Acelaphine herpesvirus.

<400> 53

aagtaataga	actatactct	agagaagaga	agaggatgag	cactgcattt	gatatacgaga	60
ccatgtttag	agaatacaca	tactacacac	agagggtcac	tggcctgcgg	aggacttga	120
cagaccttagc	tacaaacaga	aatcaattt	tagatgcctt	tggcagcctc	atggacgact	180
tgggggtcgt	ggggaaaacg	gtgttgaatg	ctgtgagcag	tgtggccaca	ctcttcagct	240
ctatagtctc	aggatcatc	aatttcatta	aaaacccctt	tggggaaatg	tt	292

<210> 54

<211> 152

<212> DNA

<213> artificial

<220>

<223> Portion of Acelaphine herpesvirus.

<400> 54

tgtgtccgtg	agcagcacccg	agcctctctc	atgtgaaacg	agctaagcaa	aatcaaccct	60
accagtgtga	tgagctctat	atacgggcgg	ccagtatctg	ccaaaagaat	tggagatgt	120
atatctgtct	ctcaactgtgt	ggtggtgac	ca			152

<210> 55

<211> 793

<212> PRT

<213> artificial

<220>

<223> Portion of Acelaphine herpesvirus.

<400> 55

Lys Gly Ile His Ser Asp Pro Ser Ala Phe Pro Phe Arg Val Cys Ser

1

5

10

15

Ala Ser Asn Ile Gly Asp Ile Phe Arg Phe Gln Thr Ser His Ser Cys
20 25 30

Pro Asn Thr Lys Asp Lys Glu His Asn Glu Gly Ile Leu Leu Ile Phe
35 40 45

Lys Glu Asn Ile Val Pro Tyr Val Phe Lys Val Arg Lys Tyr Arg Lys
50 55 60

Ile Val Thr Thr Ser Thr Ile Tyr Asn Gly Ile Tyr Ala Asp Ala Val
65 70 75 80

Thr Asn Gln His Val Phe Ser Lys Ser Val Pro Ile Tyr Glu Thr Arg
85 90 95

Arg Met Asp Thr Ile Tyr Gln Cys Tyr Asn Ser Leu Asp Val Thr Val
100 105 110

Gly Gly Asn Leu Leu Val Tyr Thr Asp Asn Asp Gly Ser Asn Met Thr
115 120 125

Val Asp Leu Gln Pro Val Asp Gly Leu Ser Asn Ser Val Arg Arg Tyr
130 135 140

His Ser Gln Pro Glu Ile His Ala Glu Pro Gly Trp Leu Leu Gly Gly
145 150 155 160

Tyr Arg Arg Arg Thr Thr Val Asn Cys Glu Val Thr Glu Thr Asp Ala
165 170 175

Arg Ala Val Pro Pro Phe Arg Tyr Phe Ile Thr Asn Ile Gly Asp Thr
180 185 190

Ile Glu Met Ser Pro Phe Trp Ser Lys Ala Trp Asn Glu Thr Glu Phe
195 200 205

Ser Gly Glu Pro Asp Arg Thr Leu Thr Val Ala Lys Asp Tyr Arg Val
210 215 220

Val Asp Tyr Lys Phe Arg Gly Thr Gln Pro Gln Gly His Thr Arg Ile
225 230 235 240

Phe Val Asp Lys Glu Glu Tyr Thr Leu Ser Trp Ala Gln Gln Phe Arg
245 250 255

Asn Ile Ser Tyr Cys Arg Trp Ala His Trp Lys Ser Phe Asp Asn Ala
260 265 270

Ile Lys Thr Glu His Gly Lys Ser Leu His Phe Val Ala Asn Asp Ile
275 280 285

Thr Ala Ser Phe Tyr Thr Pro Asn Thr Gln Thr Arg Glu Val Leu Gly
290 295 300

Lys His Val Cys Leu Asn Asn Thr Ile Glu Ser Glu Leu Lys Ser Arg
305 310 315 320

Leu Ala Lys Val Asn Asp Thr His Ser Pro Asn Gly Thr Ala Gln Tyr
325 330 335

Tyr Leu Thr Asn Gly Gly Leu Leu Leu Val Trp Gln Pro Leu Val Gln
340 345 350

Gln Lys Leu Leu Asp Ala Lys Gly Leu Leu Asp Ala Val Lys Lys Gln
355 360 365

Gln Asn Thr Thr Thr Thr Thr Thr Arg Ser Arg Arg Gln Arg
370 375 380

Arg Ser Val Ser Ser Gly Ile Asp Asp Val Tyr Thr Ala Glu Ser Thr
385 390 395 400

Ile Leu Leu Thr Gln Ile Gln Phe Ala Tyr Asp Thr Leu Arg Ala Gln
405 410 415

Ile Asn Asn Val Leu Glu Glu Leu Ser Arg Ala Trp Cys Arg Glu Gln
420 425 430

His Arg Ala Ser Leu Met Trp Asn Glu Leu Ser Lys Ile Asn Pro Thr
435 440 445

Ser Val Met Ser Ser Ile Tyr Gly Arg Pro Val Ser Ala Lys Arg Ile
450 455 460

Gly Asp Val Ile Ser Val Ser His Cys Val Val Val Asp Gln Asp Ser
465 470 475 480

Val Ser Leu His Arg Ser Met Arg Val Pro Gly Arg Asp Lys Thr His
485 490 495

Glu Cys Tyr Ser Arg Pro Pro Val Thr Phe Lys Phe Ile Asn Asp Ser
500 505 510

His Leu Tyr Lys Gly Gln Leu Gly Val Asn Asn Glu Ile Leu Leu Thr
515 520 525

Thr Thr Ala Val Glu Ile Cys His Glu Asn Thr Glu His Tyr Phe Gln
530 535 540

Gly Gly Asn Asn Met Tyr Phe Tyr Lys Asn Tyr Arg His Val Lys Thr
545 550 555 560

Met Pro Val Gly Asp Val Ala Thr Leu Asp Thr Phe Met Val Leu Asn
565 570 575

Leu Thr Leu Val Glu Asn Ile Asp Phe Gln Val Ile Glu Leu Tyr Ser
580 585 590

Arg Glu Glu Lys Arg Met Ser Thr Ala Phe Asp Ile Glu Thr Met Phe
595 600 605

Arg Glu Tyr Asn Tyr Tyr Thr Gln Arg Val Thr Gly Leu Arg Arg Asp
610 615 620

Leu Thr Asp Leu Ala Thr Asn Arg Asn Gln Phe Val Asp Ala Phe Gly
625 630 635 640

Ser Leu Met Asp Asp Leu Gly Val Val Gly Lys Thr Val Leu Asn Ala
645 650 655

Val Ser Ser Val Ala Thr Leu Phe Ser Ser Ile Val Ser Gly Ile Ile
660 665 670

Asn Phe Ile Lys Asn Pro Phe Gly Gly Met Leu Leu Phe Gly Leu Ile
675 680 685

Ala Ala Val Val Ile Thr Val Ile Leu Leu Asn Arg Lys Ala Lys Arg
690 695 700

Phe Ala Gln Asn Pro Val Gln Met Ile Pro Asp Ile Lys Thr Ile Thr
705 710 715 720

Ser Gln Arg Glu Glu Leu Gln Val Asp Pro Ile Ser Lys His Glu Leu
725 730 735

Asp Arg Ile Met Leu Ala Met His Asp Tyr His Ala Ser Lys Gln Pro
740 745 750

Glu Ser Lys Gln Asp Glu Glu Gln Gly Ser Thr Thr Ser Gly Pro Ala
755 760 765

Asp Leu Asn Lys Ala Lys Asn Val Leu Arg Arg Arg Ala Gly Tyr Lys
770 775 780

Pro Leu Lys Arg Thr Asp Ser Phe Glu
785 790